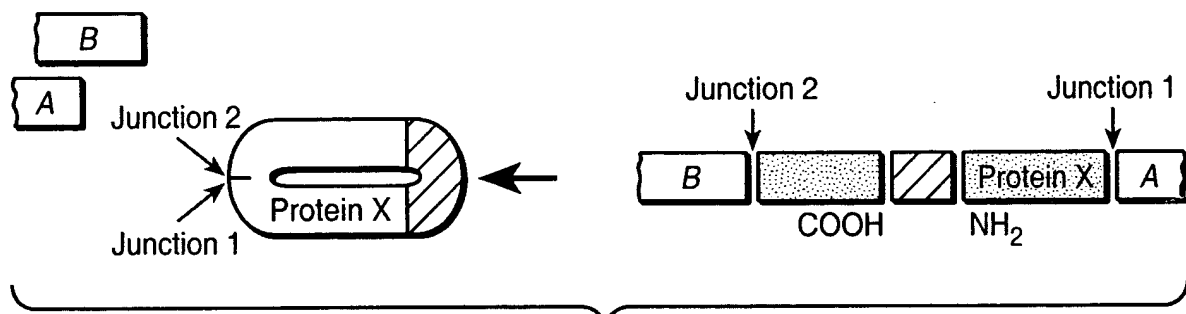


Modifications / Engineering:

- 1.) Separate Intein Domains (designated A and B)
- 2.) Reverse Translational Order
- 3.) Fuse Former C and N-termini



**FIG. 1A**

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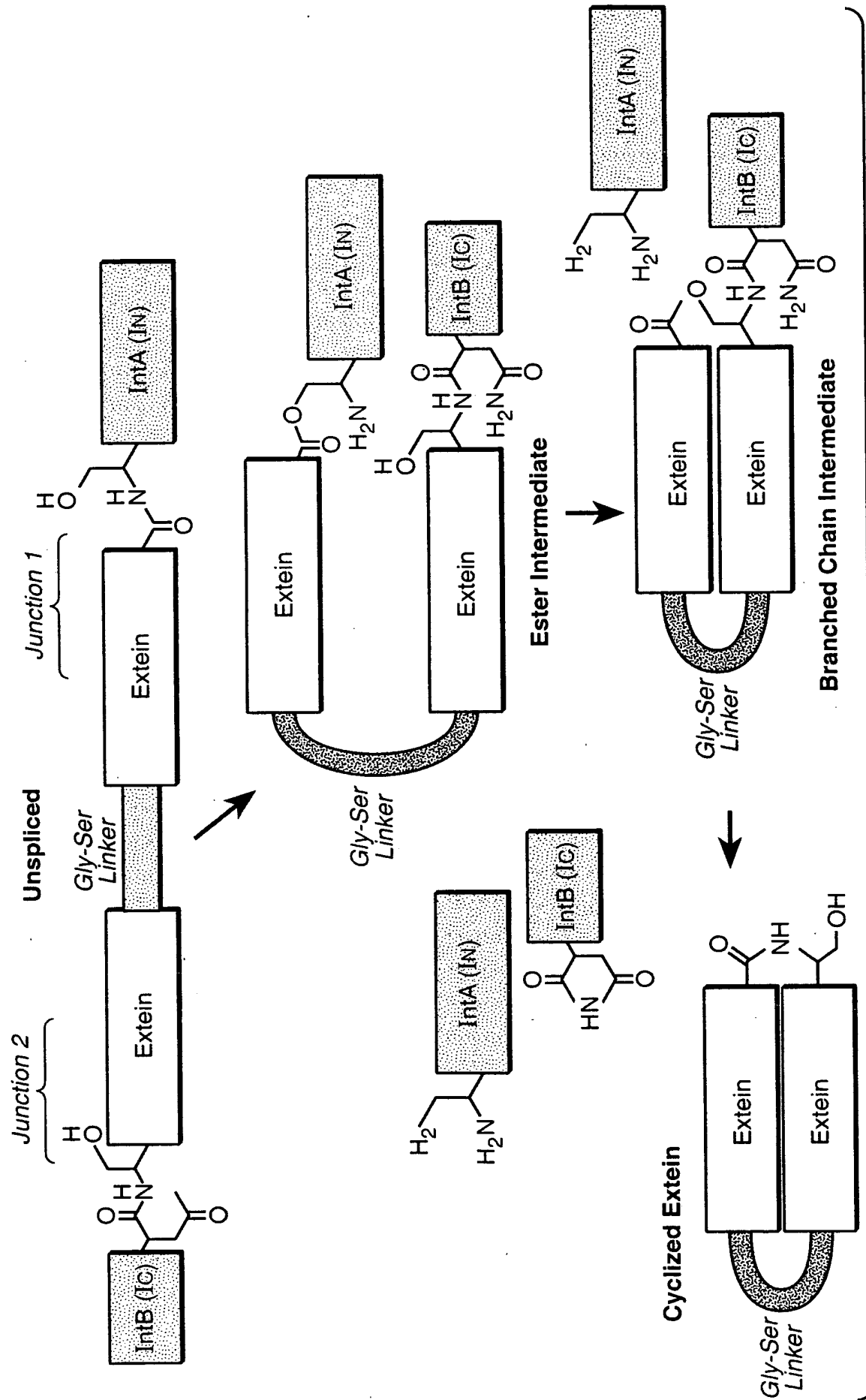
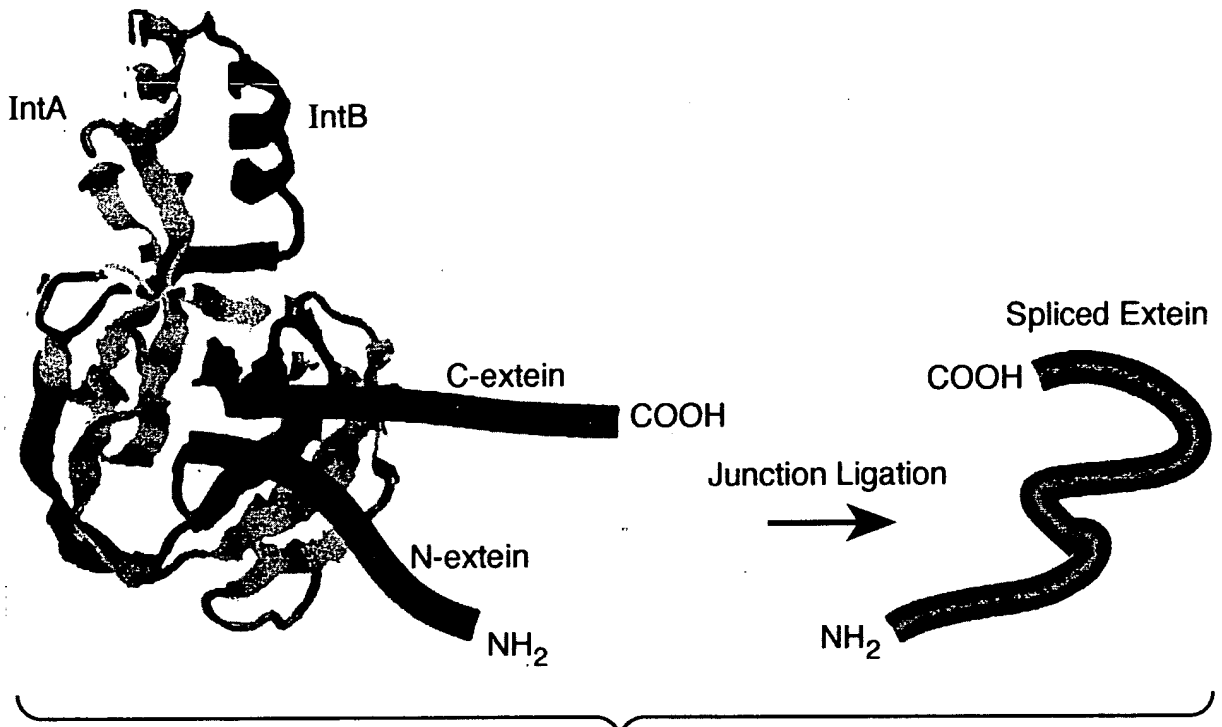
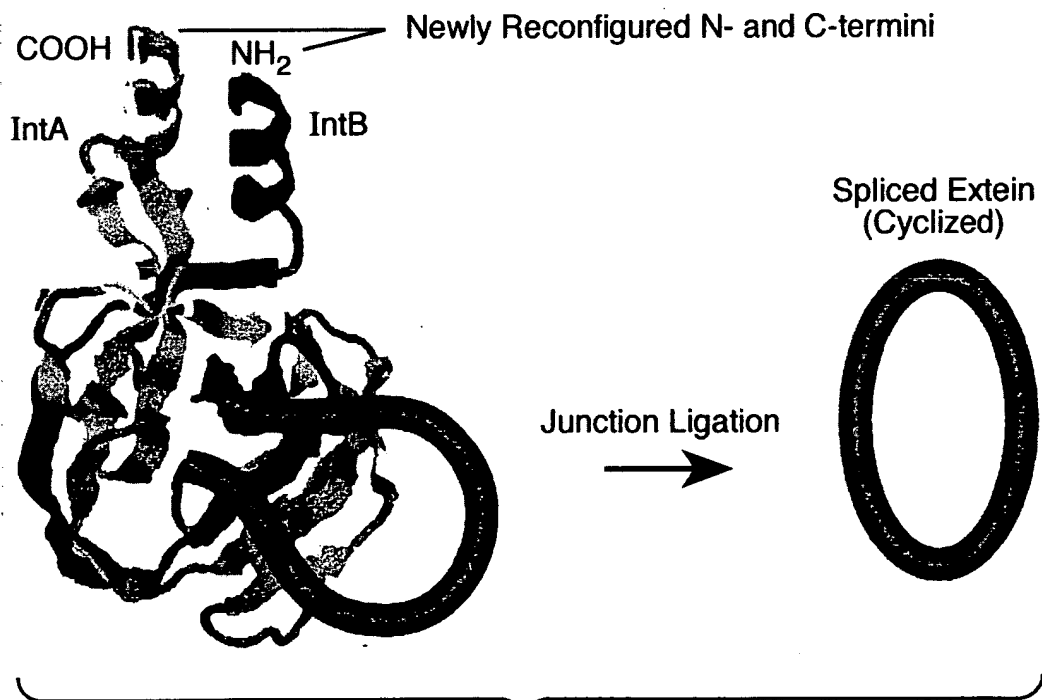


FIG..1B

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**FIG. 2A****FIG. 2B**

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GCISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVYILKT  
 RLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLMSDEELGLLGHLIGDGC  
 TLPRHAIQYTSNKIELAEKVVELAKAVFGDQINPRISQERQWYQVYIPASYRLTHNKNPIT  
 KWLENLDVFGRLSYEKFVPNQVFEQPQRAIAIFLRHLWSTDGCVKLIVEKSSRPVAYYATSS  
 EKLA KDVQSLLLKLG INARLSKISQNGKGRDNYHVTITGQADLQIFVDQIGAVDKDKQASVE  
 EIKTHIAQH QANTNRDVIPKQIWKTYVLPQIQIKGITTRDLQMLRGNA YCGTALYKHNL SRE  
 RAAKIATITQSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNS

**FIG.\_3A**

YCITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLD RHGNPVLADRLFHSGEHPVYTV  
 RTVEGLRVGTANHP LLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQSAFSVDCAGFARGKPE  
 FAPTTYTVGVPGLVRFLEAHRDPDAQAIADELTDGRFYAKVASVTDAGVQPVYSLRVDTA  
 DHAFITNGFVSHNT

**FIG.\_3B**

ECLTSDHTVLTTRGWIPIADVTLDDKVAVLDNNTGEMSYQNPQKVHKYDIEGPMYEVKTAGV  
 DLFVTPNHRMYVNTTNNTTNQYNLVEASSIFGKKVRYKNDAIWNKTDYQFILPETATLTGH  
 TNKISSTPAIQPEMNAWLTF FGLWIANGH TT KIAEKTAENNQKQRYKVILTQVKEDVCDII  
 EQTLNKLGFNFIRSGKDYTIENKQLWSYLNPF DN GALNKYLPDWVWELSSQQCKILLNSLCL  
 GNCLFTKNDDTLHYFSTSERFANDVSRLALHAGTTSTIQLEAAPS NLYDTIIGLPVEVNTTL  
 WRVIINQSSFYSYSTD KSSALNLSNNVACYVNAQSALTLEQNSQKINKNTLVLTKNNVKSQT  
 MHSQRAERVD TALLTQKELDNSLNHEILINKNPGTSQLECVVNPEVNNTSTNDRFVYYKGPV  
 YCLTGPNNVFYVQRNGKAVWTGNS

**FIG.\_3C**

LCVAPETMILTEDGQFFIKDLEGKIIKVWNGNEFSSVTVVKTGTEKELLEVELSNGCTL SCT  
 PEHKFIIVKSYTEAKKQKTDDNAI ANAERVDAQDLKPRMKLIKFDLPTLFGNSEHDIKYPYT  
 HGFFCGDGTYTKYGKPQLSLYGDKKELLTYLDVRTMTGLE DASGR LNTWLPLDLAPKFDVPI  
 NSSLECRM EWLAGYLDADGCVFRNGT NESIQVSCIHLDFLKRIQLLLIGMGVTSKITKLHDE  
 KITTMPDGKGGQKPYSCKPIWRLFISSSGLYHLSEQGFETRRLKWEPRQPQRNAERFVEVLK  
 VNKTGRVDDTYCFTEPINHAGVFNGILTQC

**FIG.\_3D**

GCFTKGTQVMMADGADKSIESIEVGDKVMGKDGM PREVVGLPRGYDDMYKVRQLSSSTRNAK  
 SEGLMDFTVSADHKLILKTKQDVKIATR KIGGNTYTGVTFYVLEKTKTGIELVKAKTKVFGH  
 HIHGQNGAE EKAATFAAGIDSKEYIDWII EARDYVQVDEIVKTSTTQMINPVHFESGKLG NW  
 LHEHKQNKSLAPQLGYLLGTWAGIGNVKSSAFTMNSKDDVKLATRIMNYSSKLGMTCSSTES  
 GELNVAENEEFFNNLGAEKDEAGDFTFDEFTDAMDEL TINVHGAAASKKNLLWNALKSLG  
 FRAKSTDIVKSIPQHIAVDDIVVRESLIAGLVDAAGNVETKSNGSIEAVVRTSFRHVARGLV  
 KIAHSLGI ESSINIKDTHIDAAGVRQEFACIVNLTGAPLAGVLSKALARNQTPVVKFTRDP  
 VLFNFDLIKSAKENYYGITLAEETHQFLLSNMALVHNC

**FIG.\_3E**

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GCLSYATNQPYFLKSDNVNFSKLTSLKVSNNHYILSATLELLIPFQYNRIYPIVSLIKRELQT  
GYKVYELDFYISVIVSTVEHYVLTNGWKRIELTVDDLVATLDIQYLIYNNTEVDLFSSN  
VIFSSVINLICMNRINVYDFWIPKTNNFFVNALLVHNS

**FIG.\_3F**

GCISKFSHIMWSHVSKPLFNFSIKKSHMHNFNKNYIQLLDQGEAFISRQDKKTTYKIRTNSE  
KYLELTSNHKILTLRGWQRCDQLLCNDMITTQIGFELSRKKKYLLNCIPFSLCNFETLANIN  
ISNFQNVFDFAANPIPNIANNIIVHNS

**FIG.\_3G**

GCFAGGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKS  
DSSREVPPELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELV  
KEVSKSYPISEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYE  
NDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAELN  
LCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNTEPLWDAIVGLGFLKDGVKNIPIPSFLST  
DNIGTRETFLAGLIDSDGYVTDEHGKATIKTIHTSVRDGLVSLARSLGLVSVNAEPAKVD  
MNGTKHKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAFARECRGFYFELQELKEDDYG  
ITLSDSDHQLLANQVVHNC

**FIG.\_3H**

GCFAYGTRGALADGTTEKIGKIVNQMDVEVMSYDPDQVVPKVVNWFNNGPAEQFLQFT  
VEKSGGNGKSQFAATPNHLIRTPAGWTEAGDLVAGDRVMAAEPHRLSDQQFQVVLGSLMGDG  
NLSPNRRDRNGVRFRMGHGAKQVDYLQWKTALLGNIKHSTHVNDKGATFVDFTPPLPELAELQ  
RAVYLGDKKKFLSEENFKALTPLALVFWMDDGPFTVRSKGLQERTAGGSGRIEICVEAMSE  
GNRIRLRDYLDRDTHGLDVRLRLSGAAGKSVLVFSTASSAKFQELVAPYITPSMEYKLLPRFR  
GQGAVTPQFVEPTQRLVPARVLDVHVKPHTRSMNRFDIEVEGNHNYFVDGVMVHNS

**FIG.\_3I**

YCLSFTEILTVEYGPLPIGKIVSEEINCSVYSVDPEGRVYTQAIQWHDGRGEQEVLEYELE  
DGSVIRATSDHRFLTDDYQLLAIEEIFARQLDLLTLENIKQTEEALDNHRLPFPLLDAGTIK

**FIG.\_3J**

KALALDTPLPTPTGWTAMGDVAVGDELLAVDEAPTRVVAATEVMLGRPCYEIEFSDGTVIVA  
DAQHQWPTSYGIRTSQALRCGLDIIAAAGSTPRHAGRLTTAAAFMAPVLCIDSVRRVRSVPVR  
CVEVDNAAHLYLAGRGMVPTHNS

**FIG.\_3K**

GALAYDEPIYLSDGNIINIGEFVDKFFKKYKNSIKKEDNGFGWIDIGNENIYIKSFNKLSLI  
IEDKRILRVWRKKYSGKLIKITTKNRREITLTHDHPVYISKTEVLEINAEMVKVGDIYIIP  
KNNTINLDEVIKVETVDYNGHIYDLTVEDNHTYIAGKNEGFAVSNC

**FIG.\_3L**

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GALYDFSVIQLSNGRFVLIGDLVEELFKKYAEKIKTYKDLEYIELNEEDRFEVSVSPD1KA  
 NKHVVSrvWRRKVREGEKLIRIKTRTGNEIILTRNHPLFAFSNGDVVRKEAEKLVGDRVAV  
 MMRPPSPPPQTKAVVDPAIYVKISDYLVPNKGKMIKVPNDGIPPEKAQYLLSVNSYPVKLVR  
 EVDEKLSYLAGVILGDGYISSNGYYISATFDDEAYMDAFVSVVSDFIPNYVPSIRKNGDYTI  
 VTVGSKIFAEMLSRIFGIPRGRKSMWDIPDVLSNDDLTRYFIAGLFDADGYVDENGPSIVL  
 VTKSETVARKIWIYVLQR1GIISTVSRVKSRRGFEKEGELFRVLIISGVEDLAKFAKFIPLRHSRK  
 RAKLMEILRTKKPYRGRRTYRVPISSDMIAPLRQMLGLTVAELSKLASYYAGEKVSSESLIRH  
 IEKGRVKEIRRSTLKGIALALQQIAKDVGNEEAWVRARLQ1IAEGDVYWDEVVSVEEVDPK  
 ELGIEYVYDLTVEDDHNYVANGILVSN

**FIG.\_3M**

PCVSGDTIVMTSGGPRTVAEELEGKPF TALIRGSGYPCPSGFFRT CERDVYDLRTREGHCLRL  
 THDHRVLVMDGGLWRAAGELERGDRLVMDAAGEFPALATFRGLRGAGRQDVYDATVYGAS  
 AFTANGFIVHNC

**FIG.\_3N**

GCIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESK  
 RVVKGKVNVIWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGDI  
 LIGGMPDGEDYKFIFDYWLAGFIAGDGCDFKYHSHVKGHEIYDRLRIYDYRIETFEIINDY  
 LEKTFGRKYSIQKDRNIYYIDIKARNITSHYLLKLEGIDNGIPPQILKEGKNAVLFSFIAGLF  
 DAEGHVSNNKPGIELGMVNRKLIEDVTHYLNALGIKARIREKLRKDGIDYVLHVEEYSSLLRF  
 YELIGKNLQNEEKREKLEKVL SNHKGNGFGLPLNFNAFKEWASEYGVEFKTNGSQTIAIIND  
 ERISLGQWHTRNRVSKAVLVKMLRKL YEATKDEEVKRMHLHIEGLEVV RHITTTNEPRTFYD  
 LTVENYQNYLAGENGMI FVHNT

**FIG.\_30**

NSILPEEWVPLIKNGKVKIFRIGDFVDGLMKANQGKVKTGDTEVLEVAGIHAFSFD RKSKK  
 ARVMAVKAVIRHRYSGNVYRIVLNSGRKITITEGHS LFVYRNGDLVEATGEDVKIGDLLAVP  
 RSVNLPEKRERLNIVELLNLSPEETEDIILTIPVKGRKNFFKGMLRTLRLWIFGEEKRVRTA  
 SRYLRHLENLGYIRLRKIGYDIIDKEGLEKYRTLYEKLVDVVRNGNKKREYLVFNAVRDVI  
 SLMPEEELKEWRIGTRNGFRMGTFVDIDEDFAKLLGYYVSEGSARKWKNQTTGGWSYTVRLYN  
 ENDEVLDDMEHLAKKFFGKVKRGNKYVEIPKKMAYIIFESLCGT LAENKRVPEVIFTSSKGV  
 RWAFLEGYFIGDGDVHPSKRVRLSTKSELLVNGLVLLNLSLGVSAIKLGYSGVYRVYVNEE  
 LKFTEYRKKKNVYHSHIVPKDILKETFGKVFQKNISYKKFREL VENGKLDREKAKRIEWLLN  
 GDIVLDRVVEIKREYYDGYVYDLSVDEDENFLAGFGFLYAHNS

**FIG.\_3P**

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DSVTGETEII IKRNGKVEFVAIEELFQRVDYRIGEKEYCVLEGVEALTLDNRGRLVWKSVPY  
VMRHRTNKRIYRVWFTNSWYLDVTEHSLIGYMNTSKVKPGKPLKERLVEVKPGELGESVKS  
LITPNRAIAHGIRVNPIAVKLWELIGLLVGDNWGGQSNWAKYNVGLSLGLDKEEIEEKILK  
PLKNTGIISNYDKSKKGDVSILSKWLARFMVRYFKDESGSKRIPEFMFNLPREYIEAFLRG  
LFSADGTVSLRKGVPEVRLTSVNPELSSSVRKLLWLVGVSNSMFVETNPNRYLGKESGTHSV  
HVRIKDKHRFAERIGFLLDRKATKLSENLGGHTSKKRAYKYDFDLVYPKKVEEIAIDGYVYD  
IEVEGTHRFFANGILVHNT

**FIG.\_3Q**

KCLLPEEKVVLPEIGLVTLRELFELANEVVKDEEKEVRKLGKMLTGVDERGNVKKLLNALYV  
WRVAHKGEMIRVKVNGWYSVTVTPEHPFLTNRGWVKAGELKEGDYIAIPRRVYGNEDIMKFS  
KIAKELGIKGEKEFYLAGASIDIPKVLFLAPSKLVSAFLRGYFDAKGVVRENYIEVPLFE  
DLPLLLLRFGIVSRIEKSTLKISGKRNLLEFRKHVGFTDSEKAKALDELISKAKESERYPII  
EELRRLGLLFGFTRNELRIEENPTYEVIMEILERIERGSPNLAEKIIVLEGRIKEENYLRL  
EEGLIENGKLTTELKELLEVRNRNREFDSKDVDYVRNIVENLVFLPVEKVERIEYEGYVYDV  
TTETHNFVANGILVHNT

**FIG.\_3R**

QCFSGEEVIIVEKKGDRKVVKLREFVEDALKEPSGEGMDGDIKVITYKDLRGEDVRILTKDGF  
VKLLYVINKREGKQKLRKIVNLDKDYWLAVTPDHKVFTSEGLKEAGEITEKDEIIRVPLVILD  
GPKIASTYGEDGKFDDYIRWKKYEKTGNGYKRAAKELNIKESTLRWWTQGAKPNSLKMIEE  
LEKLNLLPLTSEDSRLEKVAILGALFSDGNIDRNFNLTLSFISSEKAIERFVETLKELFGE  
FNYEIRDNHESLGKSILFRTWDRRIIRFFVALGAPVGNKTKVKLELPWWIKLKPSLFLAFMD  
GLYSGDGSVPRFARYEEGIKFNGTFEIAQLTDDVEKKLPFFEEIAWYLSFFGIKAKVRVDKT  
GDKYKVRLLIFSQSIDNVNLFLEFIPISLSPAKREKFLREVESYLAAPPESSLAGRIEELREH  
FNRIKKGERRSFIETWEVVNVNTYNVTTETGNLLLANGLFFVKN

**FIG.\_3S**

LCLTPDTYVVLGDGRIETIEDIVNAKERNVLSLDLNLISIKIDTAIKFWKLRYNGLSKITL  
SNNYELKATPDHCLLVLRDNQLKWIPAKDIKENDYIAMPFNYKVERKPISSLNLLKYLDITD  
VLIEFDENSTIFEKIAEYIRNNIKTSTKYKYLNRNRVPLKYLIEWNFDLDEIEKEAKYIYKS  
VAGTKKIPLFKLDERFWYFAGLVLDGDSIQDSKIRIAQTPLKDVKSILDETFFPLHNWISGN  
QVIISNPIIAEILEKLGMRNGKLNIIIFSLPESYINALIAGYFDTDGCFSLLYDKKAKKHNL  
RMVLTSKRRDVLEKIGIYLNLSIGILNTLHKSREVYSIIISNKSLETTFKEKIAKYLKIRKEAF  
INGYKTYKKEHEERFECDLLPVKEVFKKLTFEKGRKEILKDSKIHENWYKEKTNNIPREKL  
KTVLRYANNSEHKEFLEKIVNGDISFVRVKKVENIPYDGYVYDLSIKHNQNFISNGVISHNC

**FIG.\_3T**

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KCLTGD TKVIANGQLFELRELVEKISGGKFGPTPVKGLKVIGIDEDGKLREFEVQYVYKDKT  
 ERLIRIRTRLGRELKVTPYHPLLVNRRNGEIKWVKAELKPGDKLAVPRFLPIVTGEDPLAE  
 WLG YFLGGGYADSKENLIMFTNEDPLLQRFMELTEKLFSDARIREITHENGTSKVYVNSKK  
 ALKLVNSLGNNAHIPKECWGRGIRSF LRAYFDCNGGVKGNAIVLATASKEMSQEIAYALAGFGI  
 ISRIQEYRVIIISGSDNVKKFLNEIGFINRNKLEKALKLVKKDDPGHDGLEINYELISYVKDR  
 LRLSFFNDKRSWSYREAKEISWELMKEIYYRLDELEKLKESLSRGILIDWNEVAKRIEEVAE  
 ETGIRADELLEYIEGKRKLSFKDYIKIAKVLGIDVEHTIEAMRVFARKYSSYAEIGRRLGTW  
 NSSVKTILESNAVNVEILERIRKIELELIEEILSDEKLKEGIAYLIFLSQNELYWDEITKVE  
 ELRGEFIIYDLHVPGYHNF IAGNMPTVVHNT

**FIG.\_3U**

SCVTGDTKVYTPDEREVKIRDFMNYFENGLIKEVSNRIGRDTVIAAVSFNSRIVGHPVYRLT  
 LESGRIIEATGDHMF LTPEGWKQTYDIKEGSEVLVKPTLEGTPYEPDPRVIIDIKEFYNFLE  
 KIEREHN LKPLKEAKTFRELITKDEKILRRALELRAEIEENGLTKREAEILELISADTWIPR  
 AELEKKARISRTRLNQILQRLEKKGYIERRIEGRKQFVRKIRNGKILRNAMDIKRILEEEFG  
 IKISYTTVKLLSGNVDMAYRILKEVKEKWLVRDDEKAGILARVVGFI LGDGH LARNGRI  
 WFNSSKEELEMLANDLRKLGLKPSEIIERDSSSEIQGRKVKGRIMLYVDNAAFHALLRFWK  
 VEVGNKTKKGYTVPEWIKKGNLFVKREFLRGLFGADGTPCGKRYNFNGIKLEIRAKKESLE  
 RTVEFLNDVADLLREFDVDSKITVSPTKEGFIIRLIVTPNDANYLNFLTRVGYAYAKDTYAR  
 LVGEYIRIKLAYKNIILPGIAEKAIELATVTNSTYAAKVLGVSRDFVVRNLKGTQIGITRDF  
 MTFEEFMKERV LNGYVIEKVIKKEKLG YLDVYDVT CARDHSFISNGLVSHNC

**FIG.\_3V**

NCLTSNSKILTDDGYIYIKLEKLKEKLDLHIKIYNTEEGEKSSNLFVSERYADEKIIIRIKTE  
 SGRVLEGSKDHPVLT LN GYVPMGMLKEGDDVIVYPYEGVEYEEPSDEIILDEDDFAEYDKQI  
 IKY LKDRGLLPLRMDNKNIGIIARLLGFAGDGSIVKENGDRERLYVAFY GKRET LIKIRE  
 LEKLG IKASRIYSRKREVEIRNAYGDEYTS LCEDNSIKITSKAFALFMHKLGMPIGKKTEQI  
 YKIPEWIKKAPKWVKNRFLAGLFGADGSRAVFKNYTPLPINLTMSKSEELKENILEFLNEIK  
 LLLAEFDIESMIYEIKSLDGRVSYRLAIVGEESIKNFLGRINYEYSGEKKVIGLLAYEYLRR  
 KDI AKEIRKKCIKRAKELYKKGVTVSEMLKMDEF RNEFISKRLIERAVYENLDEDDVRISTK  
 FPKFEEFIEKYGVIGGFVIDKIKEIEEISYDSKLYDVGVISKEHNF IANSIVVHNC

**FIG.\_3W**

KCVDGDTLVLTKEFGLIKIKELYEKLDGKGRKIVEGNEEWTELEKPITVYGYKDGKIVEIKA  
 THVYKGVSSGMVEIRTRTGRKIKVTP IHR LFTGRVTKDGLILKEVMAMHVKPGDRIAVVKKI  
 DGGEYIKLDSSNVGEIKVPEILNEELAEFLGYLMANGTLKSGIIEIYCDDESLLERVNSLSL  
 KLFVGVGGRIVQKVDGKALVIQSKPLVDVLRRLGVPEDKKVENWKVPRELLLSPSNVVRAVFN  
 AYIKGKEEVEITLASEEGAYELSYLFAKLG IYVTISKSGEYKVRVSRGNLDTIPVEVNGM  
 PKVLPYEDFRKFAKSIGLEEVAENHLQHIIIFDEVIDVRYIPEPQEVYDVT TETHNFVGGNMP  
 TLLHNT

**FIG.\_3X**



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*Intein B*

MESG[SPEIEKLSQSDIYWDSIVSITETGVVEVFDLTVPGPHNFVAND

*Cyclid Insert (With Flagg Epitope)*

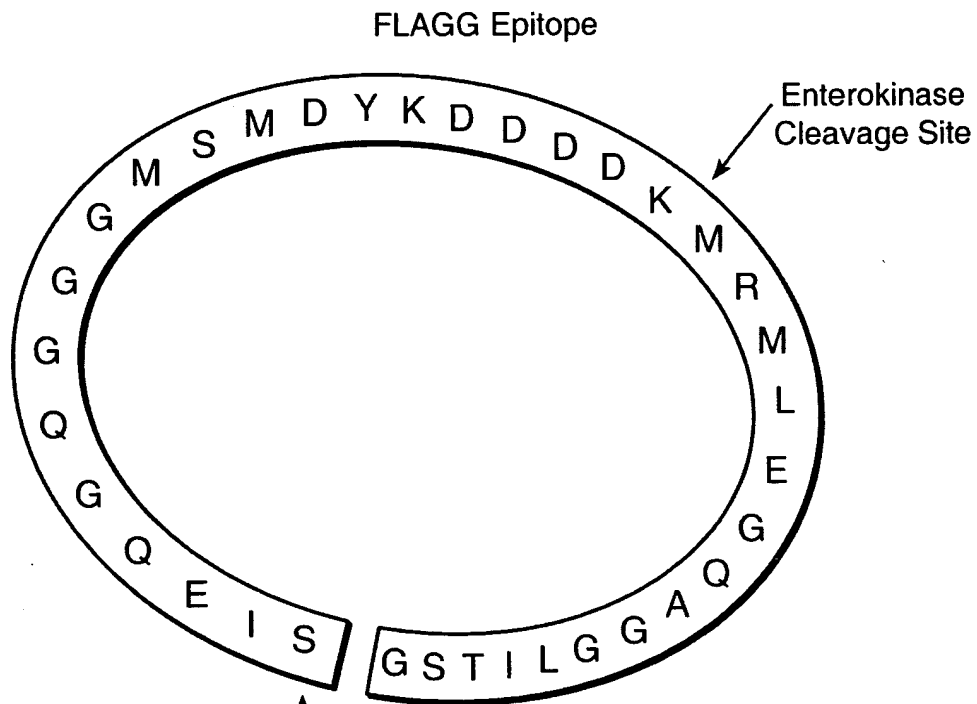
IIVHN[SIEQGQGGGMSMDYKDDDDKMRMLEGQAGGLITSG[CIS

GDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESKVS RVFCT

*Intein A*

GKKLVYILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRK

LESSSLQLS IHGYH



This is the only Invariant Extein-encoded Amino Acid  
(Depending on Intein used this can be a Cysteine, Serine or Theronine).

**FIG. 4A**

CMV Promoter →

1 / 1 31 / 11  
GCT TCG CGA TGT ACG GGC CAG ATA TAC GCG TTG ACA TTG ATT ATT GAC TAG TTA TTA ATA  
121 / 41 151 / 51  
TAC GGT AAA TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT AAT  
241 / 81 271 / 91  
TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA AGT GTA TCA TAT GCC AAG TAC GCC CCC  
361 / 121 391 / 131  
GGA CTT TCC TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT GCG  
401 / 161 511 / 171  
CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG GCA CCA AAA TCA ACG GGA CTT TCC AAA  
601 / 201 631 / 211  
CTA TAT AAG CAG AGC TCT CTG GCT AAC TAG AGA ACC CAC TGC TTA CTG GCT TAT CGA AAT  
721 / 241 751 / 251  
CTG tcg act GGA GGA ACC ATG GAG TCC GGA tca cca gaa ata gaa aag ttg tct cag agt  
841 / 281 871 / 291  
ttg act gtg cca gga cca cat aac ttt gtc gcc aat gac atc att gtc cat aac  
961 / 321 991 / 331  
ATG ctc gag ggc caa gca ggt gga CTG ATC ACC agt TGC ATC AGT GGA GAT AGT ttg  
1081 / 361 1111 / 371  
ttt gaa ata tgg gca att aat gaa cag acg atg aag cta gaa tca gct aaa gtt agt cgt  
1201 / 401 1231 / 411  
aag gca aca gca aat cat aga ttt tta act att gat ggt tgg aaa aga tta gat gag cta  
1321 / 441 1351 / 451  
GAT cca tgg tta cca TGA caa ttg GCG GCC GCT CGA GTC TAG AGG GCC CGC GGT TCG AAG  
1441 / 481  
ATC ACC ATT GAG TTT AAA CCC GCT GAT

FIG..4B-1

61 / 21	91 / 31	GTA ATC AAT TAC GGG GTC ATT AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT
181 / 61	211 / 71	GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG TCA ATG GGT GGA CTA
301 / 101	331 / 111	TAT TGA CGT CAA TGA CGG TAA ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATC
421 / 141	451 / 151	GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG GGG ATT TCC AAG TCT
541 / 181	571 / 191	ATG TCG TAA CAA CTC CGC CCC ATT GAC GCA AAT AGG CGG TAG GCG TGT ACG GTG GGA GGT
661 / 221	691 / 231	TAA TAC GAC TCA CTA TAG GGA GAC CCA AGC TGG CTA GTT AAG CTT cct ata cta gga GAT
781 / 261	811 / 271	gat att tac tgg gac tcc atc gtt tct att acg gag act gga gtc gaa gag gtt ttt gat
901 / 301	931 / 311	Flag Epitope Insert
1021 / 341	1051 / 351	IntB (Ic)
1141 / 381	1171 / 391	IntA (IN)
1261 / 421	1291 / 431	
1381 / 461	1411 / 471	

FIG..4B-2

FIG..4B

FIG..4B-1

FIG..4B-2

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTCAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCACCTCGTGACCACCCTGACCTACGGCGTGCGAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAAC TACAACAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAAC TCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5A**

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVS GEGEGDATYGKLT LKFICTT  
GKL PVPWPTLVTTLT YGVQCFS RYPDHMKQHDFFKSAMP EGYVQERTIFFKDDGNYKTRA EV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYN SHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKL VY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5B**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGTATTGACTGTGCCAGGGCCCCATA  
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
 CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
 GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
 TGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCATC  
 GTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGTATTGACTGTGCCAGGGCCCCATAA  
 CTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAGC  
 TCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
 CACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGT  
 CCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGGT  
 CGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTACC  
 GGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
 CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG  
 GCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
 AGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTA  
 CGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGA  
 AGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAC  
 GGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGGC  
 CGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTCG  
 AGCAAAAGCTGATATGCATCTCCGGAAATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAGA  
 GTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGAC  
 GATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAGCTAGTTTATA  
 TTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAaATTTTTAACTATT  
 GATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAAGAGCATATTGCTCTACCCCGTAACT  
 AGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTACG  
 CTATCGATTAA

FIG.\_5C

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTPGPHNFVANDIIVHNSEEDLGSSVQ  
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDHMLLEFVTAAGITLGMDELYKG  
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTT  
 GKLPVPWPPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
 KFE GDTLVNRIELKGIDFKEDGNILGHKLEYNYN SHNVYIMADKQKNGIKVNFKIRHNIEDL  
 EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVY  
 ILKTRLGRTIKATANHKFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
 AIDZ

FIG.\_5D

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGTATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAGTTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5E**

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEQDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAVNEQTMKLES AKVSRVFCTGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5F**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGgCcGTGCCAGGGCCCCATA  
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGACG  
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
 CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
 GGCAAGCTGCCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGACGTGCTT  
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGG  
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC  
 GAGCAAAAGCTGATATGCATCTCCGAAATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
 GCTATCGATTAA

**FIG.\_5G**

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVDLAVPGPHNFVANDIIVHNSEEDLGSSVQ  
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDHMLLEFVTAAGITLGMDELYKG  
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTT  
 GKLPVPWPPTLVTTLT YGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA EV  
 KFE GDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
 EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKKLVY  
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
 AIDZ

**FIG.\_5H**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTcCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCGAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAAC TACAACAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAAC TCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5I**

MESGSPEIEKLSQSDIYWDSIVPITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGLTLKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5J**



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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCACCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAgGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

FIG.\_5K

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPVPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKRLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

FIG.\_5L

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTCAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAAC TACAACAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAAC TCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAaATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5M**

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDMVLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGLTLKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNVIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVY  
ILKTRLGRTIKATANHKFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5N**

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
 CGTTcCTATTACGGAGACTGGAGTCGAAGAGGTTTTTTGATTTGACTGTGCCAGGGCCCCATA  
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTCAC  
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
 GGCAAGCTGCCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGG  
 CCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACCTC  
 GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
 GCTATCGATTAA

### FIG.\_50

MESGSPEIEKLSQSDIYWDSIVPITETGVVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
 GKLPVPWPPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
 KFEQDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
 EQKLICISGDSLISLASTGKRVSIDLLDEKDFEIWAINETMKLESQKVSQVSRVFCTGKKLVY  
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
 AIDZ

### FIG.\_5P

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCGAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTCAC  
CGGGGTGGTGGCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCCACCTCGTGACCACCCTGACCTACGGCGTGCGAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGTATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAGTTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5Q**

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGDSLISLASTGKRVS IKDLLDEKDFEIWAVNEQTMKLES AKVSRVFCTGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5R**

CMV Promoter →

1 / 1	31 / 11	
GCT	TGG CGA TGT ACG GGC CAG ATA TAC GCG TTG ACA TTG ATT ATT GAC TAG TTA TTA ATA	
121 / 41	151 / 51	
TAC GGT AAA TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT AAT		
241 / 81	271 / 91	
TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA AGT GTA TCA TAT GCC AAG TAC GCC CCC		
361 / 121	391 / 131	
GGA CTT TCC TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT GCG		
401 / 161	511 / 171	
CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TGG GCA CCA AAA TCA ACG GGA CTT TCC AAA		
601 / 201	631 / 211	
CTA TAT AAG CAG AGC TCT CTG GCT AAC TAG AGA ACC CAC TGC TTA CTG GCT TAT CGA AAT		
721 / 241	751 / 251	IntB (IC)
CTg tcg act GGA GGA ACC	ATG GAG TCC GGA	tca cca gaa ata gaa aag ttg tct cag agt
	M E S G	S P A N H N
841 / 281	871 / 291	
ttg act gtg cca gga cca cat aac ttt gtc gcc aat gac atc att gtc cat aac		agttATC
L T V P G P H N	F V A N	S I
961 / 321	991 / 331	
ATG ctc gag ggc caa gca ggt gga CTG ATC ACC agt		TGC ATC AGT GGA GAT AGT ttg
M L E G Q A G L I	G T S S	C I S G D S L
1081 / 361	1111 / 371	
ttt gaa ata tgg gca att aat gaa cag acg atg aag tca gct aaa gtt agt cgt		
F E I W A I N	E Q T M K A S A K V S R	
1201 / 401	1231 / 411	
aag gca aca aat cat aga ttt tta act att gat ggt tgg aaa aga tta gat gag cta		
K A T A N H R F L T I D G W K R L D E L		

FIG. 6A

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61/21	91/31	GTA ATC AAT TAC GGG GTC ATT AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT
181/61	211/71	GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG TCA ATG GGT GGA CTA
301/101	331/111	TAT TGA CGT CAA TGA CGG TAA ATG GCC ATG GCG CGC GCA TTA TGC CCA GTA CAT GAC CTT ATC
421/141	451/151	GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG GGG ATT TCC AAG TCT
541/181	571/191	ATG TCG TAA CAA CTC CGC CCC ATT GAC GCA AAT GGG CGG TAG GCG TGT ACG GTG GGA GGT
661/221	691/231	TAA TAC GAC TCA CTA TAG GGA GAC CCA AGC TGG CTA GTT AAG CTT cct ata cta gga GAT
781/261	811/271	gat att tac tgg gac tcc atc gtt tct att acg gag act gga gtc gaa gag gtt ttt gat
901/301	931/311	Flag Epitope Insert
1021/341	1051/351	IntB (Ic)
1141/381	1171/391	IntA (IN)
1261/421	1291/431	

FIG..6B

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FIG.\_6C

GAT D	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	CTG	GAG	CTG
	M	V	S	K	G	E	E	L	F	T	G	V	V	P	I	L	V	E	L
TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC
Y	G	K	L	T	L	K	F	I	C	T	T	G	K	L	P	V	P	W	P
AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC
K	Q	H	D	F	F	K	S	A	M	P	E	G	Y	V	Q	E	R	T	I
CTG	GTG	AAC	GCG	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG
L	V	N	R	I	E	L	K	G	I	D	F	K	E	D	G	N	I	L	G
AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC
N	G	I	K	V	N	F	K	I	R	H	N	I	E	D	G	S	V	Q	L
CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATC
H	Y	L	S	T	Q	S	A	L	S	K	D	P	N	E	K	R	D	H	M

TAA  
\*

```

GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC
D G D V N G H K F S V S G E G G D A T

ACC CTC GTG ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG
T L V T T L T Y G G Q C F S R Y P D H M

TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC TTC GAG GGC
F K D D G N Y K T R A E V K F E G D T

CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG
H K L E Y N Y N S H N V Y Y I M A D K Q K

GCC GAC CAC TAC CAG ACC ACC CCC ATC GGC GGC GGC CCC GTG CTG CTG CCC GAC AAC
A D H Y Q N T P I G D G G P V L L P D N

GTC CTG CTG GAG TTC GTG ACC GCC GCC GGC GGC ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG
V L L L E F V T A A A A T L L G D M D E L Y K

```

FIG.\_6D

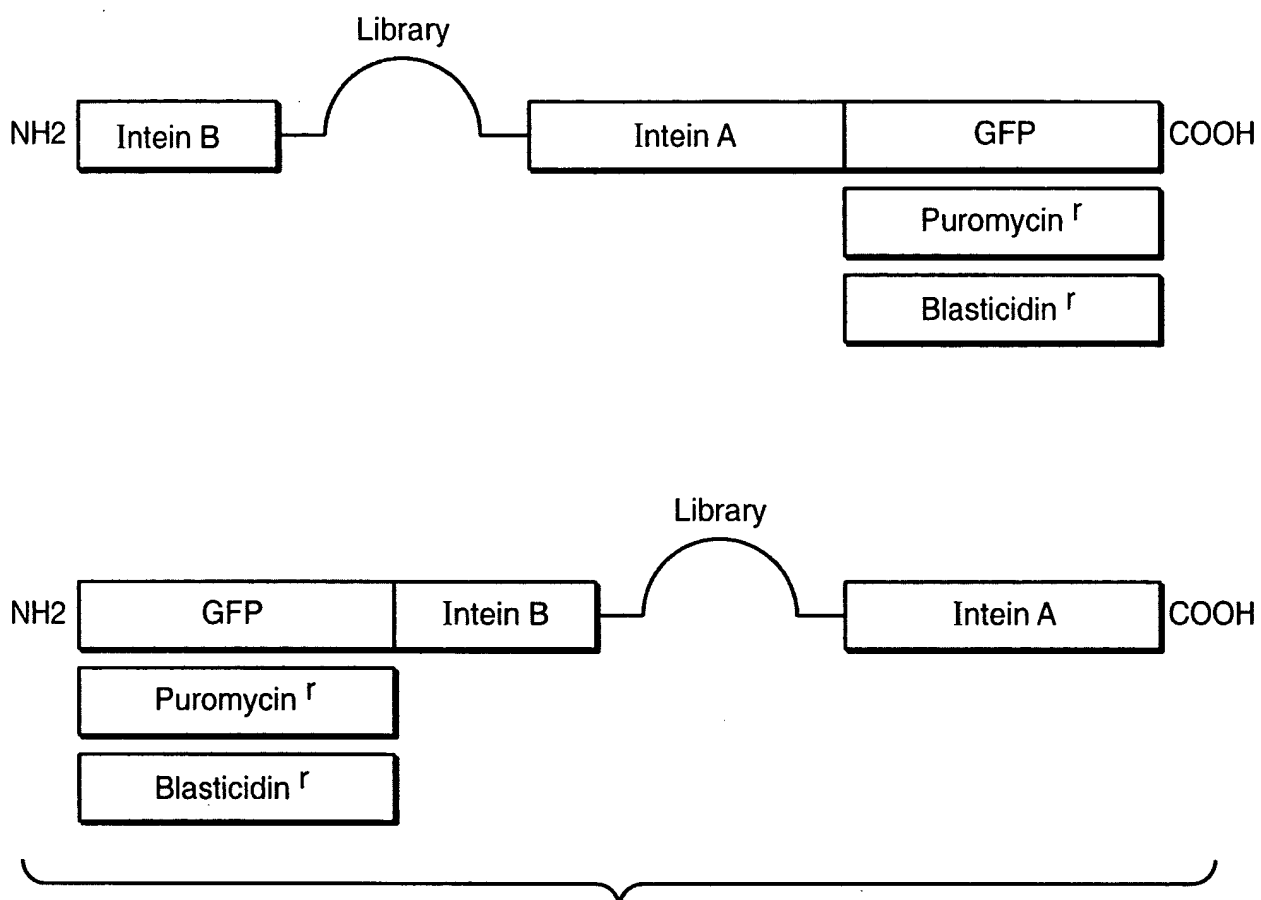
FIG.-6A	FIG.-6B
FIG.-6C	FIG.-6D

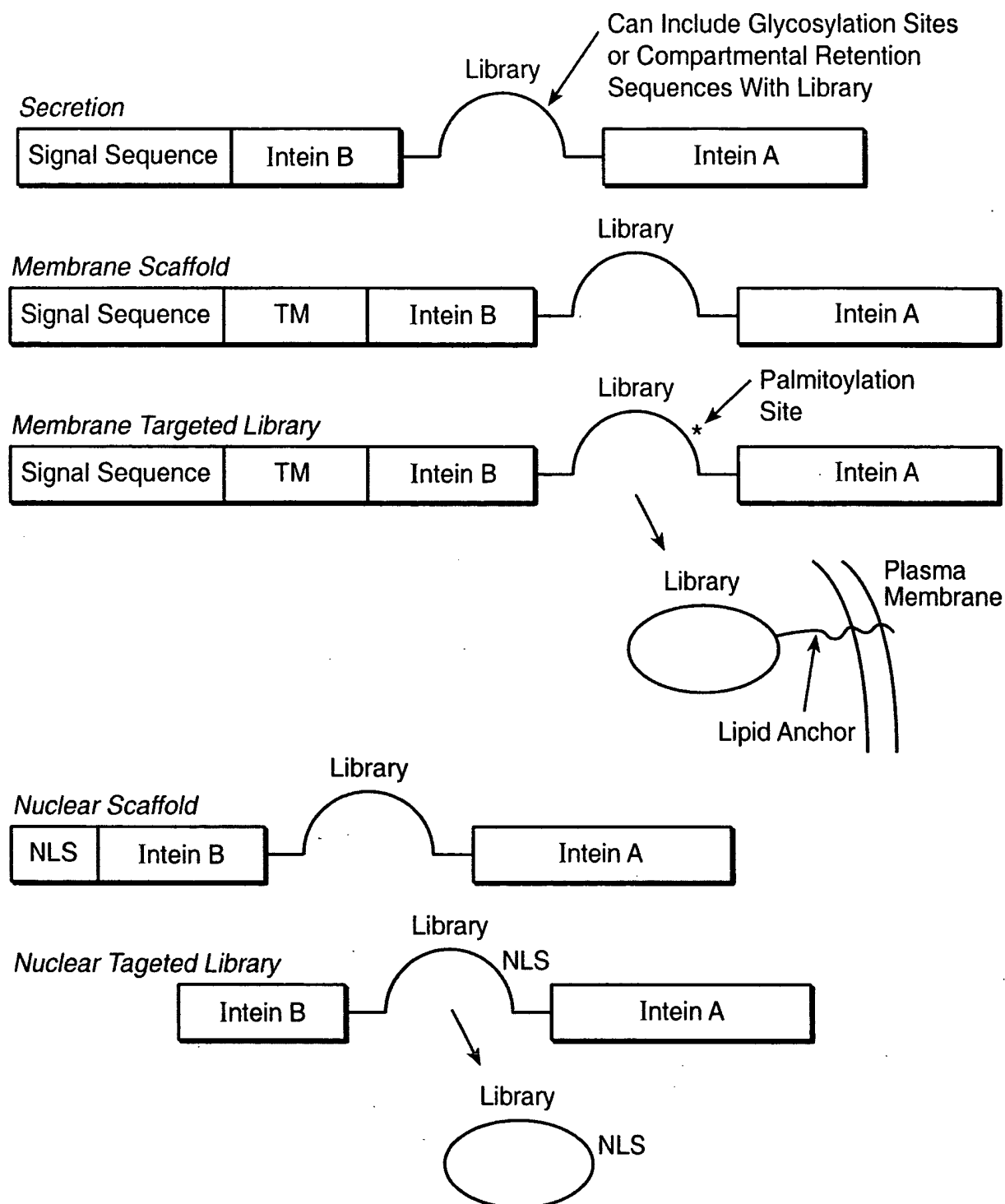
FIG.\_6



+

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**FIG..7**

**FIG.\_8**

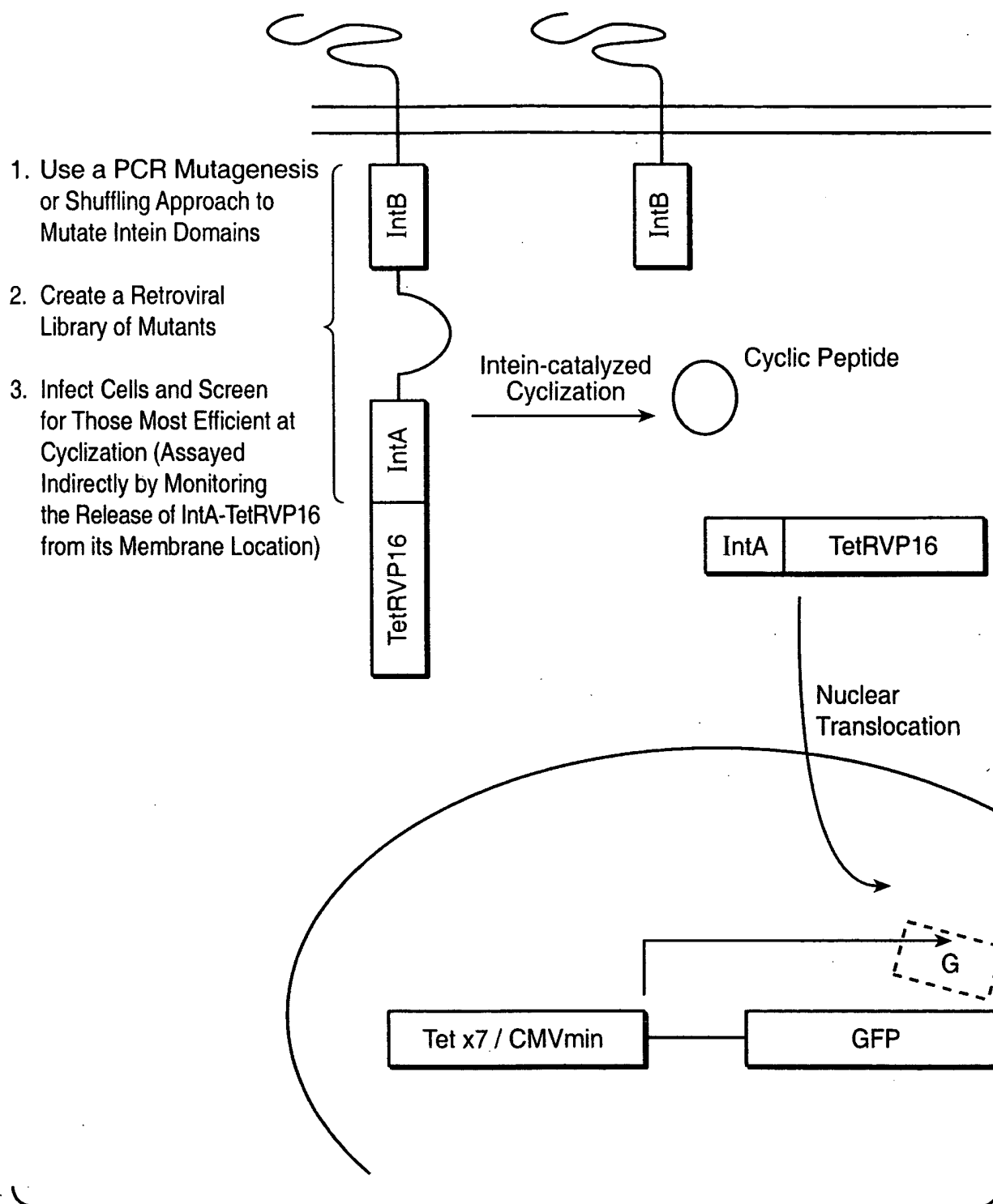
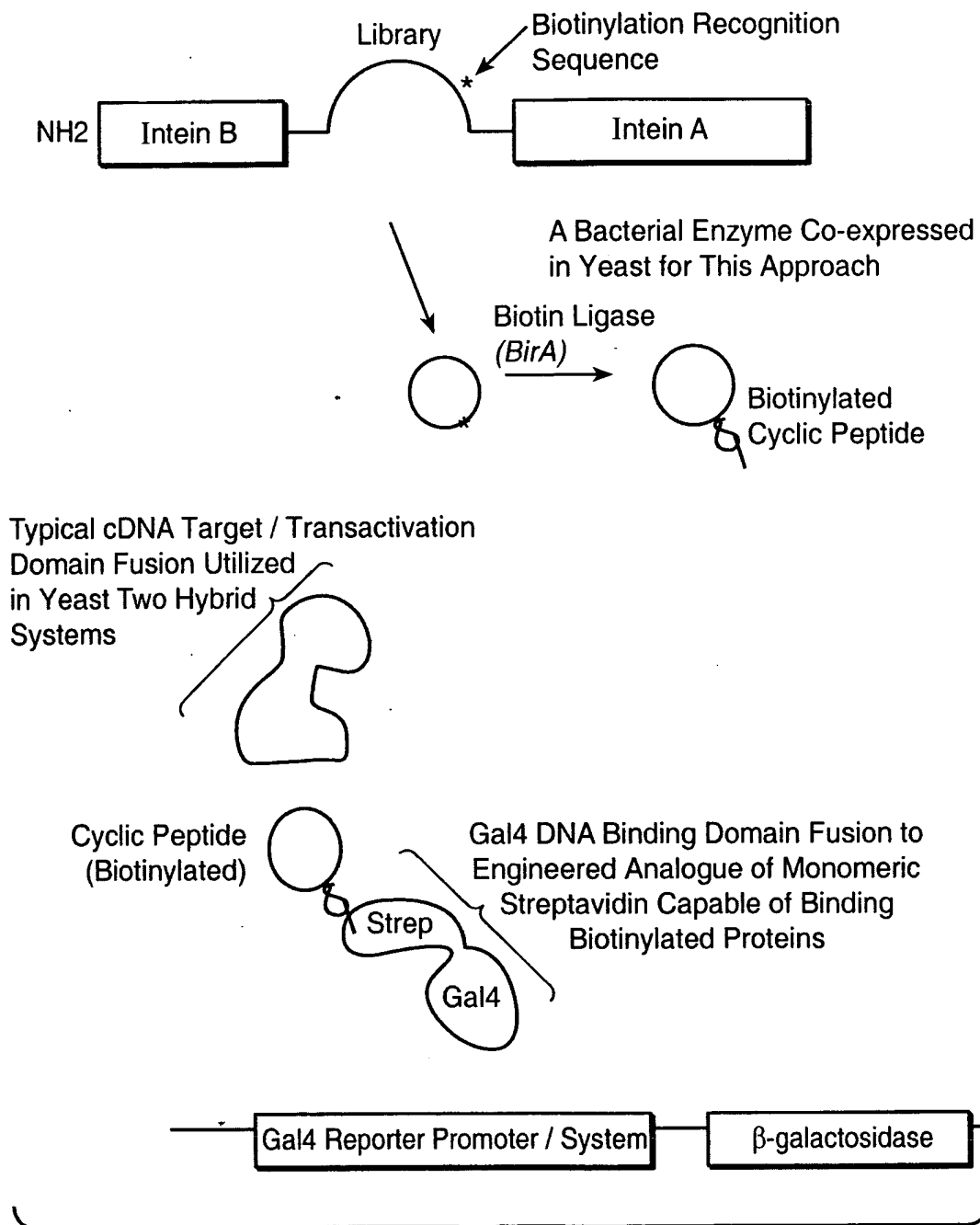
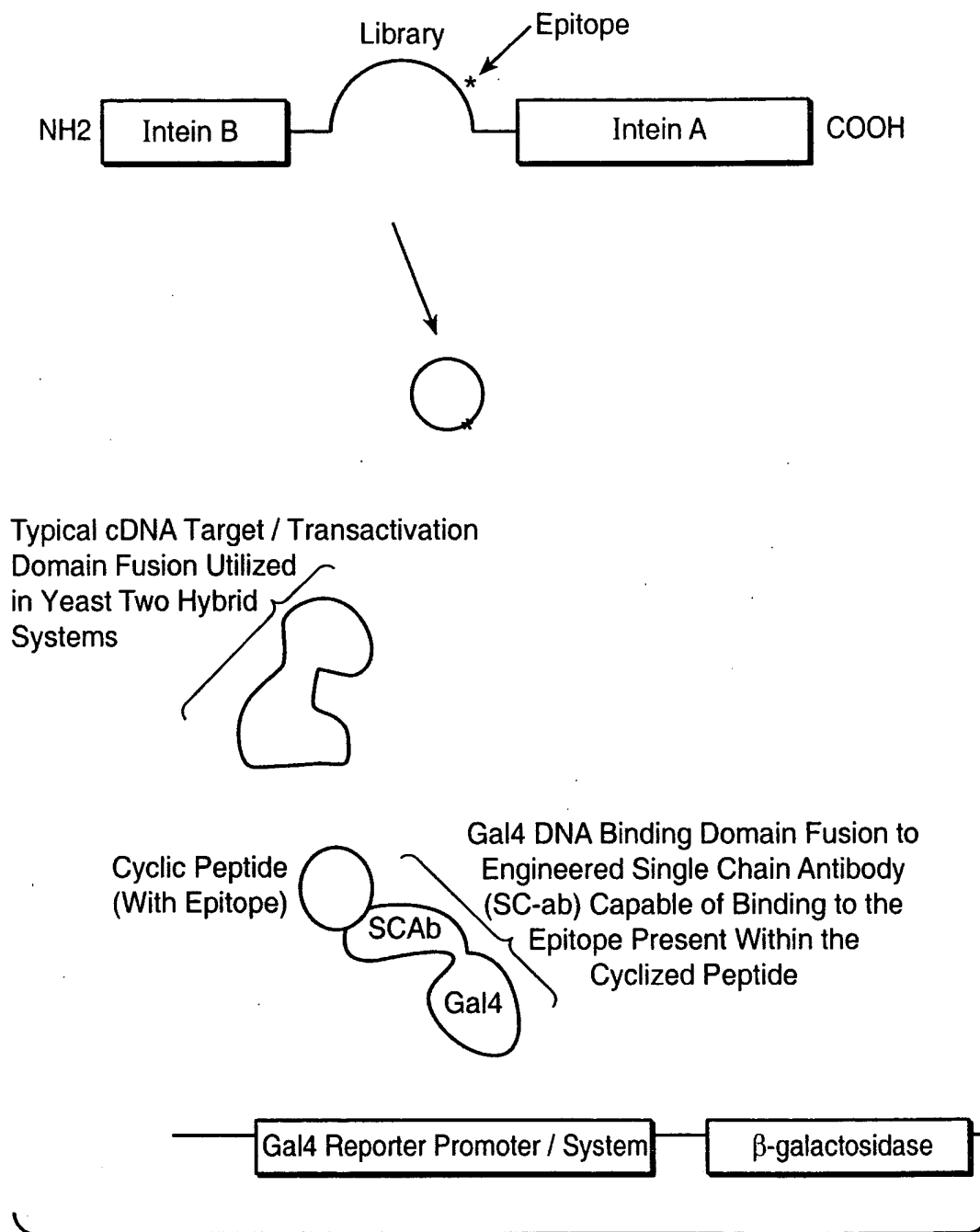


FIG. 9

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**FIG. 10**



**FIG. 11**

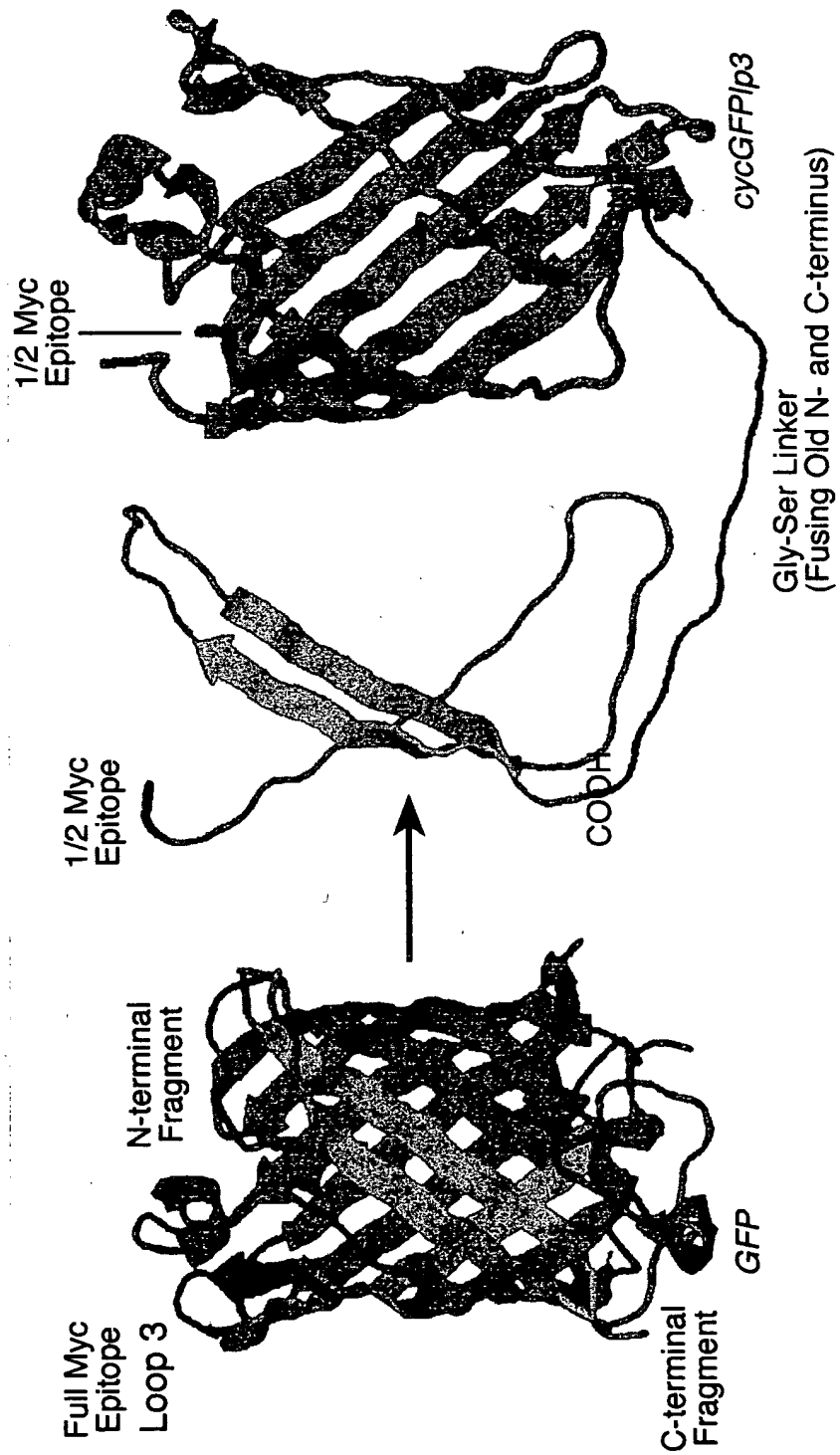


FIG. 12A

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IntB (Ic)

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGP

myc<sup>6-10</sup>HNFVANDIIVHNS~~SEEDL~~GS~~SVQLADHYQQNTPIGDGPVLL~~

PDNHYLSTQSALS KDPNEKRDMVLLFEVTAAGITLGMDE

Gly-Ser Linker

LYK~~GSNGEFSQVDKS~~MVSKGEELFTGVVPILVELDGDVNGGFP<sup>6-1-173</sup>

HKFSVSGEGEGDATYGLKTLKFICTTGKLPVPWPTLVTTL

TYGLQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDG

NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN

myc<sup>1-5</sup>YNSHNVYIMADKQKNGIKVNFKIRHNIEDL~~EQKLICISGD~~

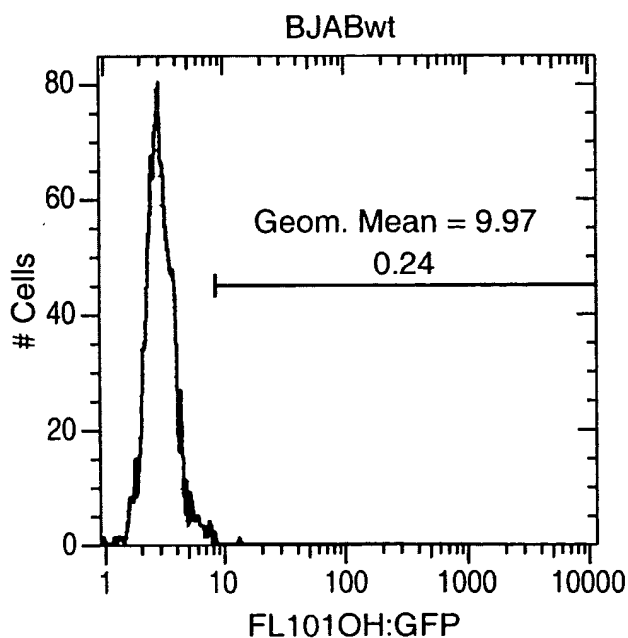
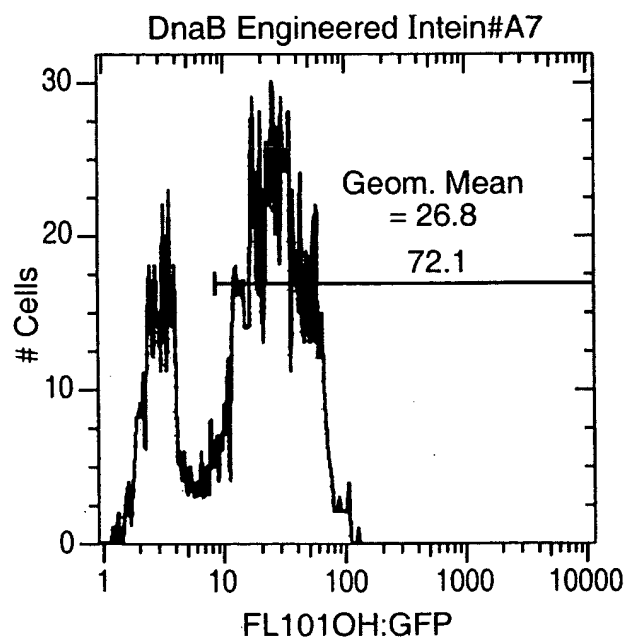
SLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKV

IntA (In)

SRVFCTGKKLVYILKTRLGRTIKATANHRFLTIDGWKRID

HA

ELSKLEHIALPRKLESSSLQLGLRGQYPYDVPDYAID

**FIG.\_12B****FIG.\_12D-1****FIG.\_12D-2**

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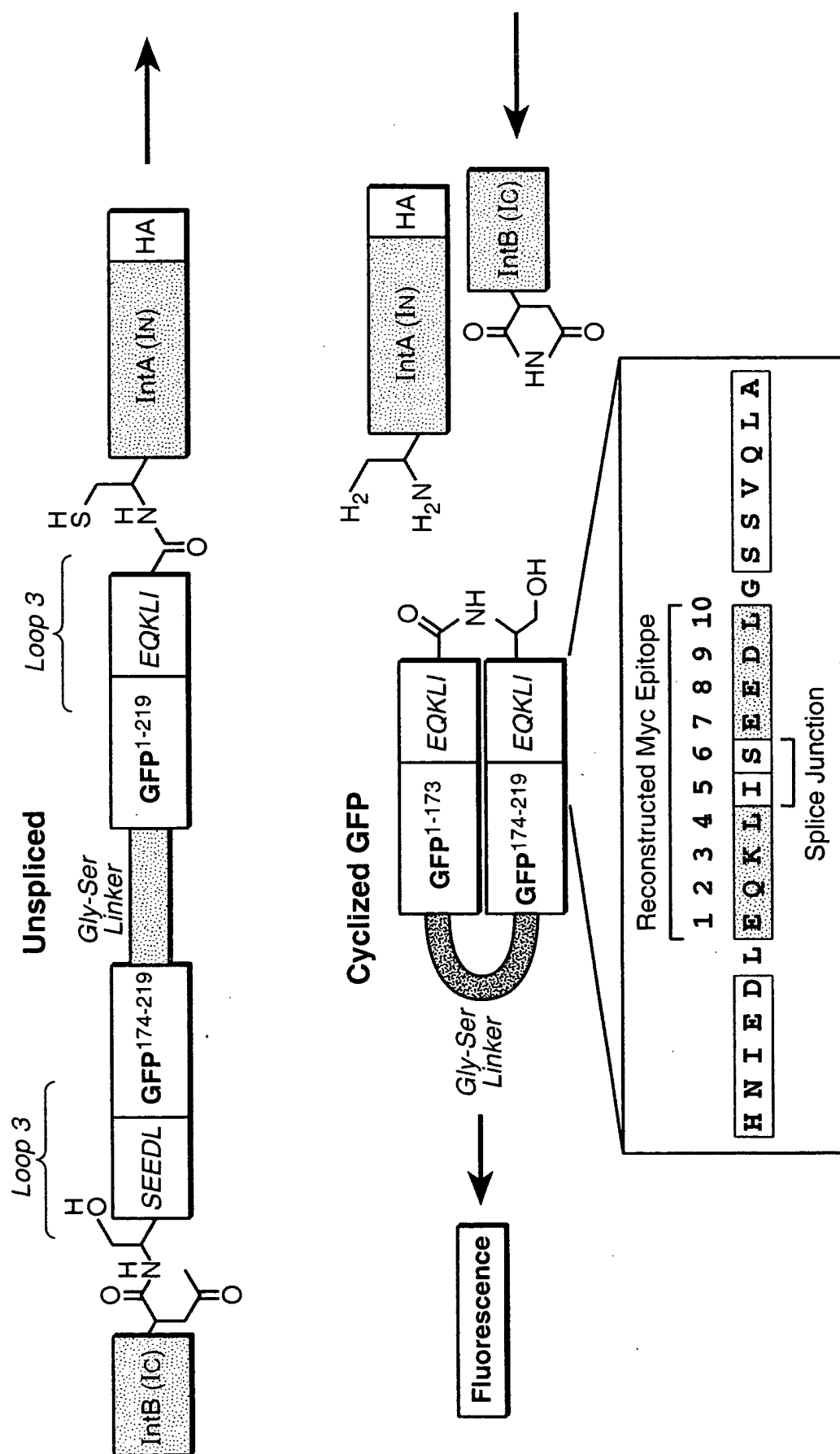
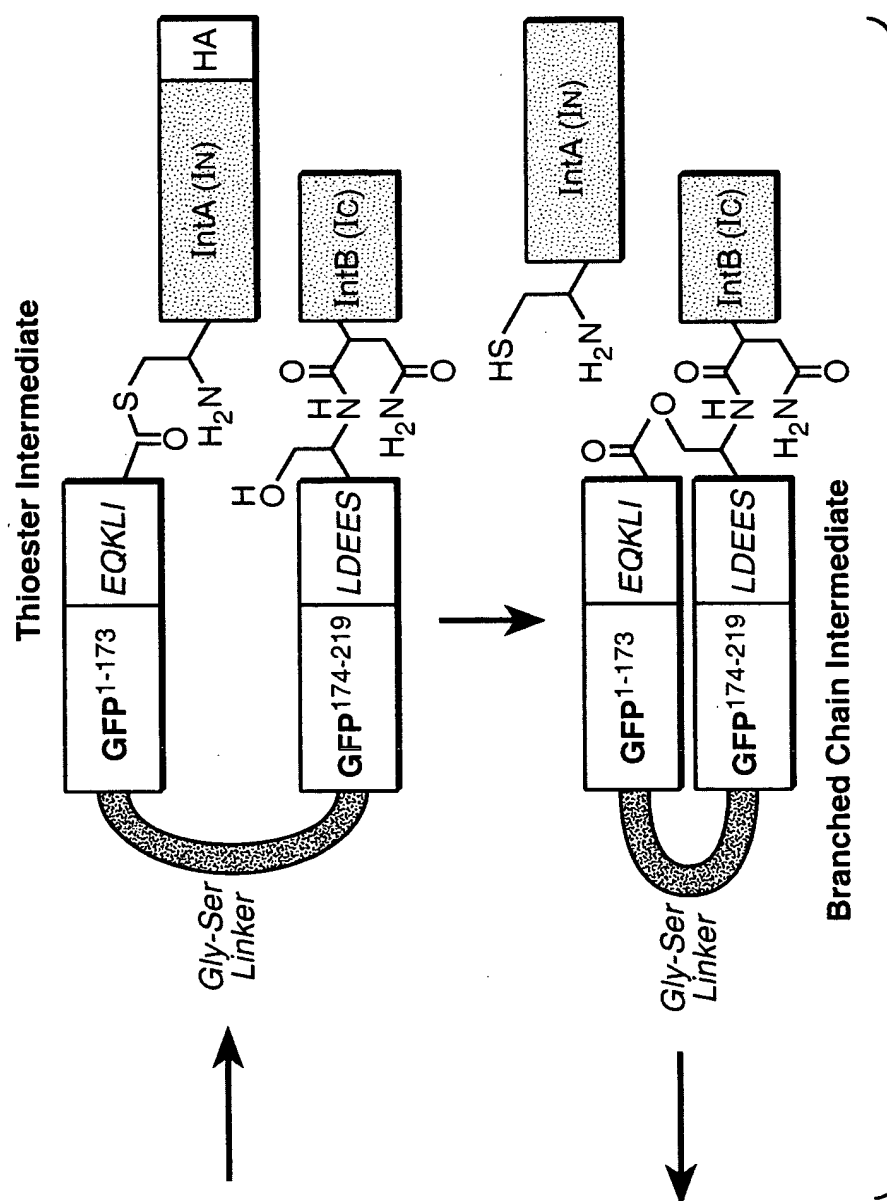


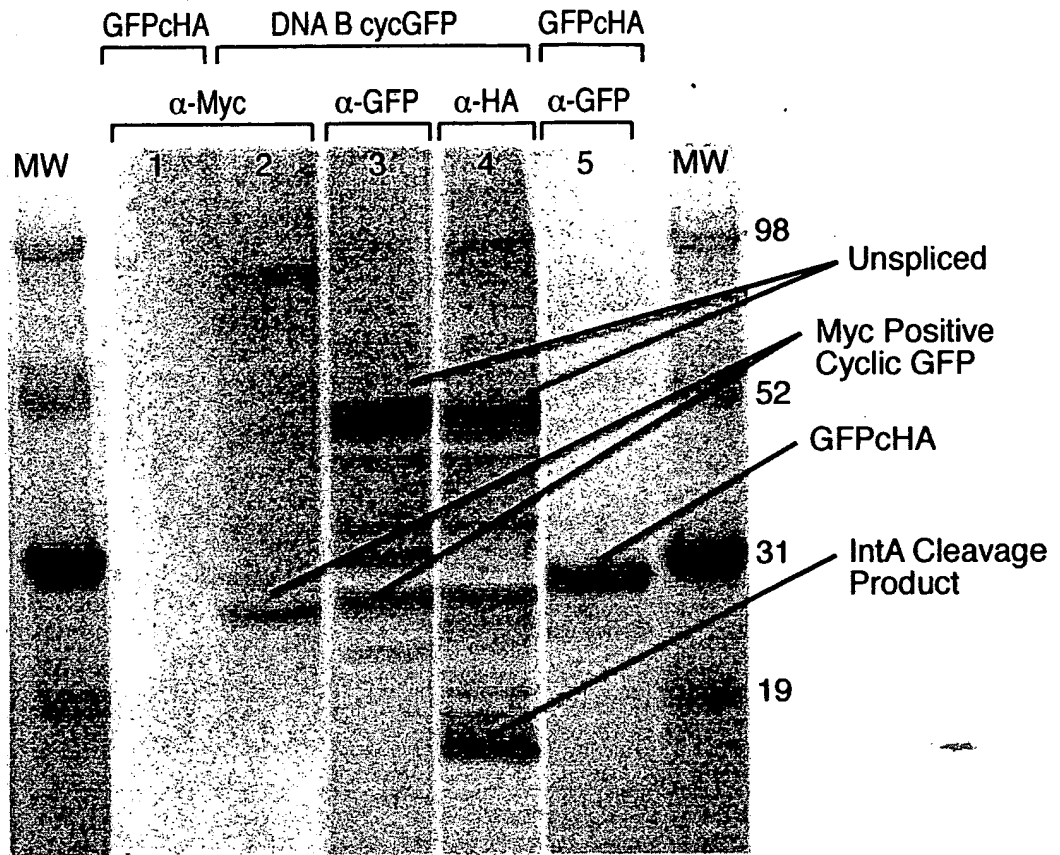
FIG..12C-1



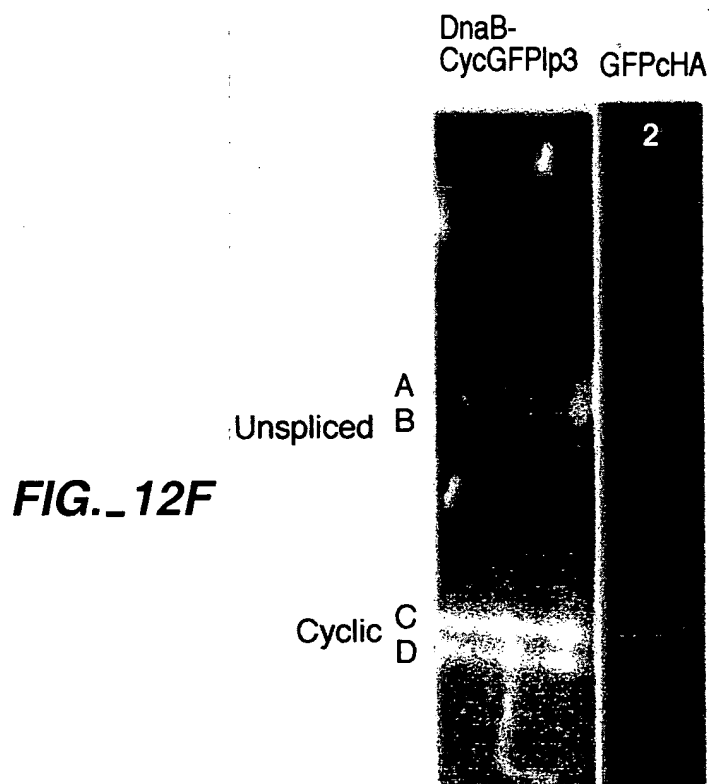


**FIG. 12C-2**

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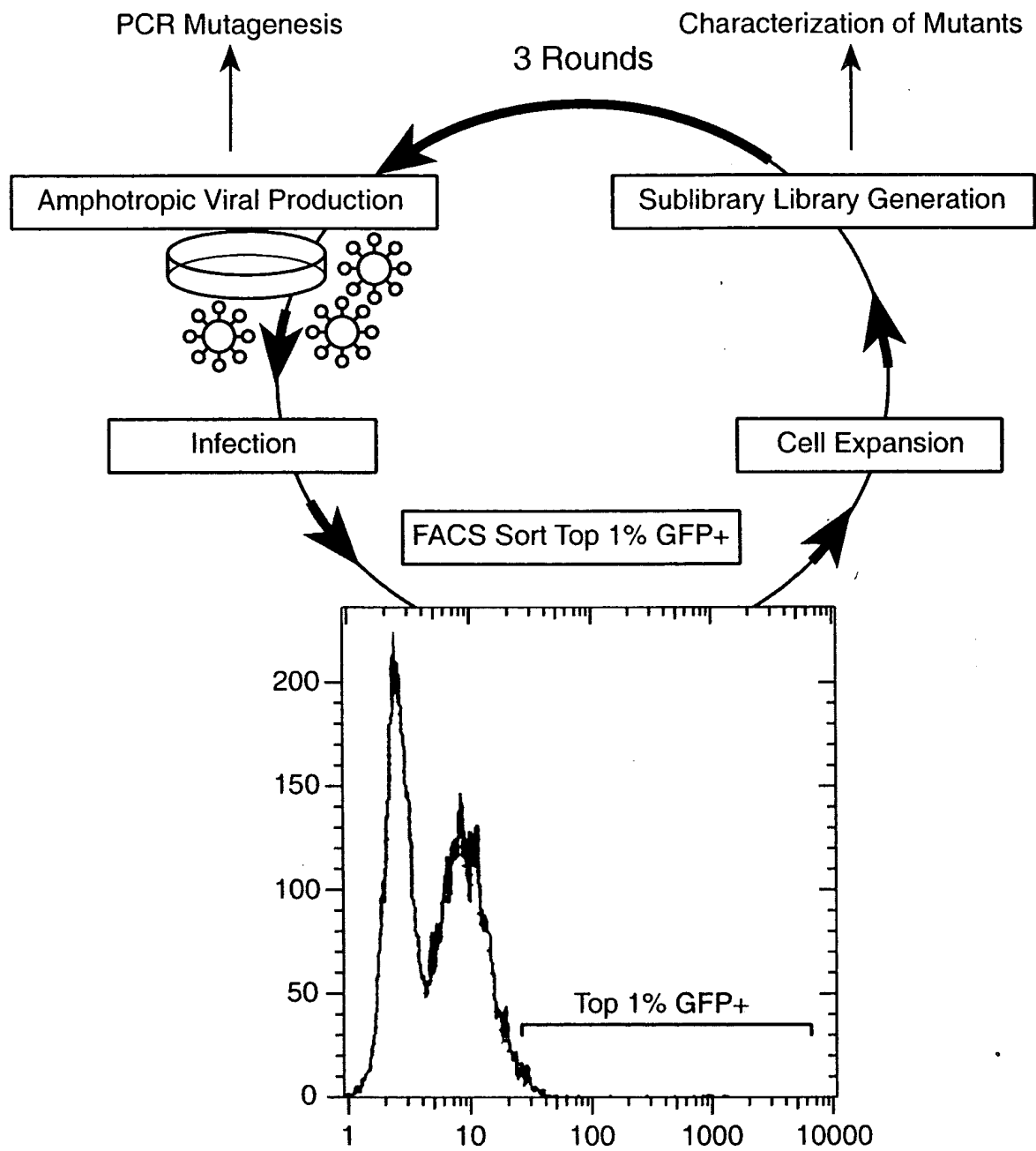


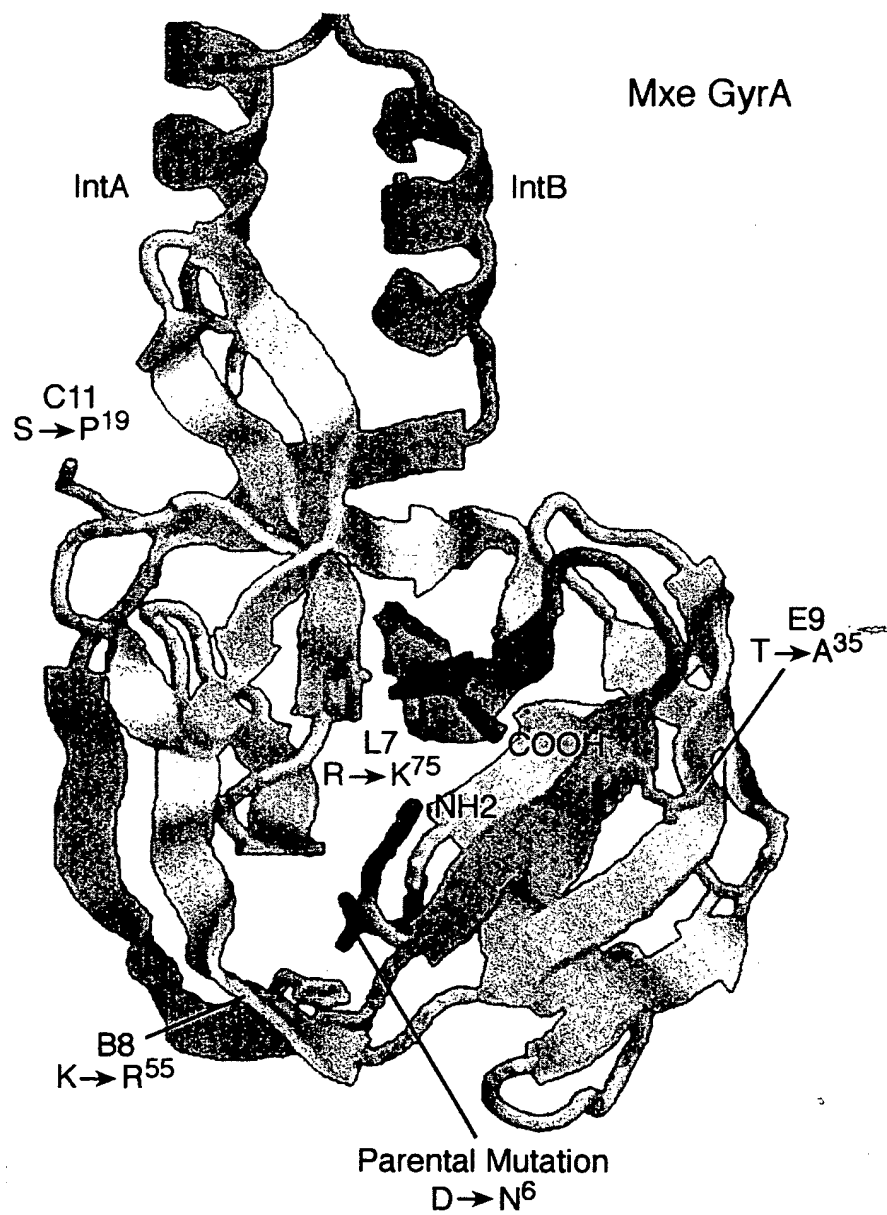
**FIG.\_12E**



**FIG.\_12F**

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**FIG.\_13A**

**FIG. 13B**

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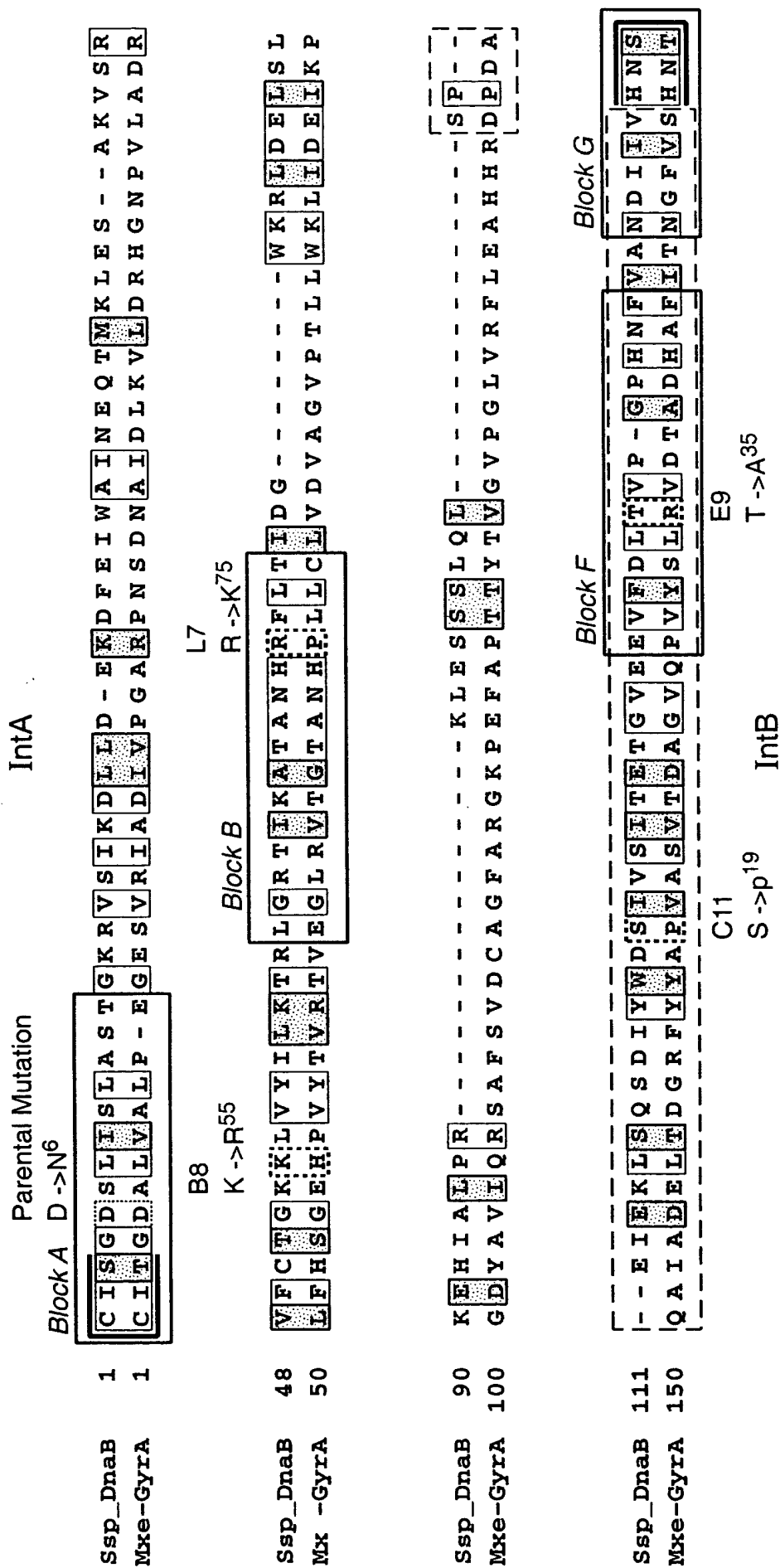
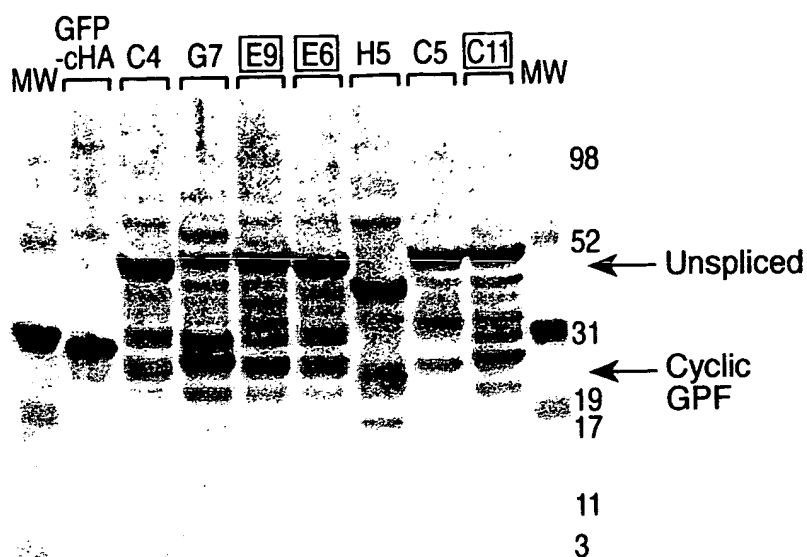
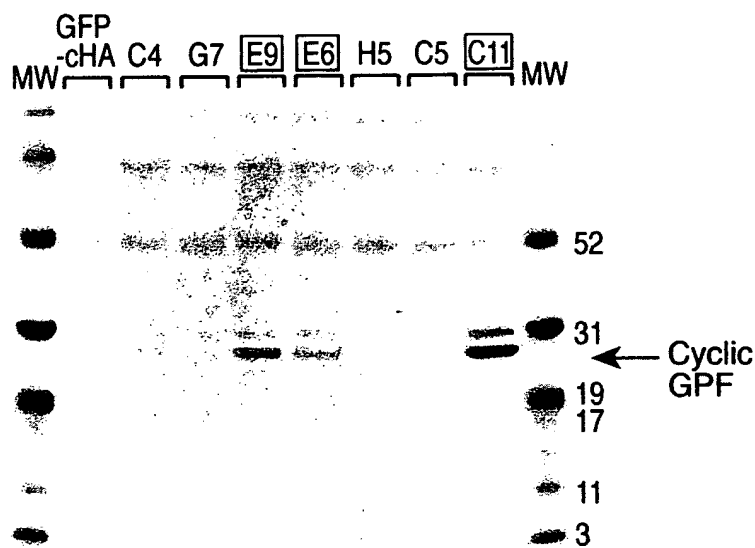


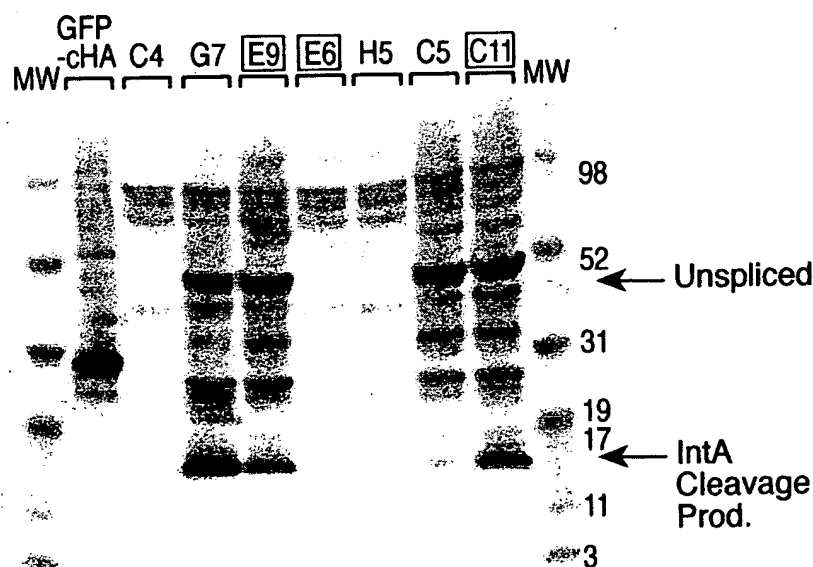
FIG.\_13C

**FIG. 13D-1**

$\alpha$ -GFP  
Identifies All Splice Intermediates and Final Product

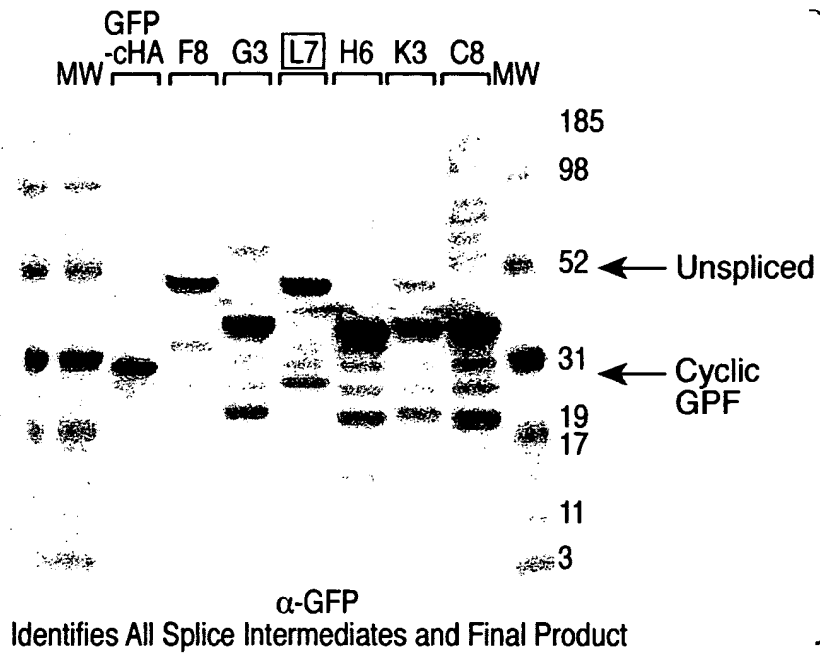
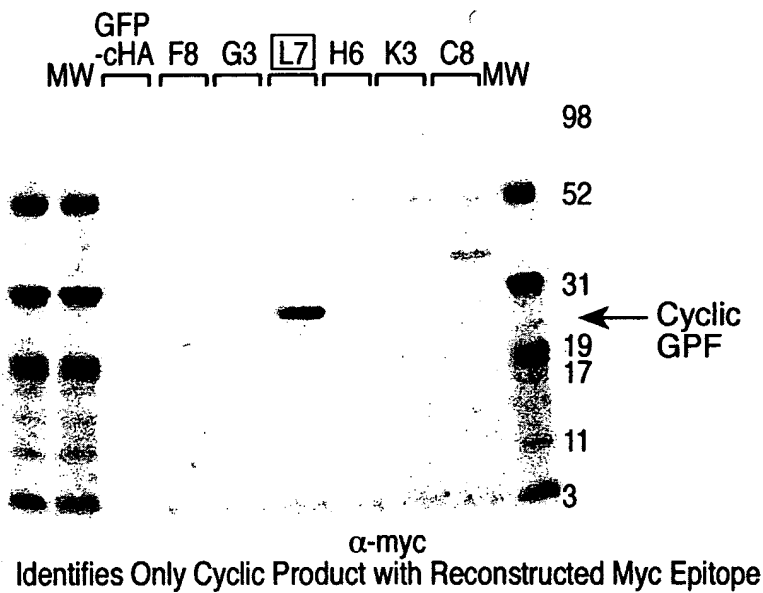
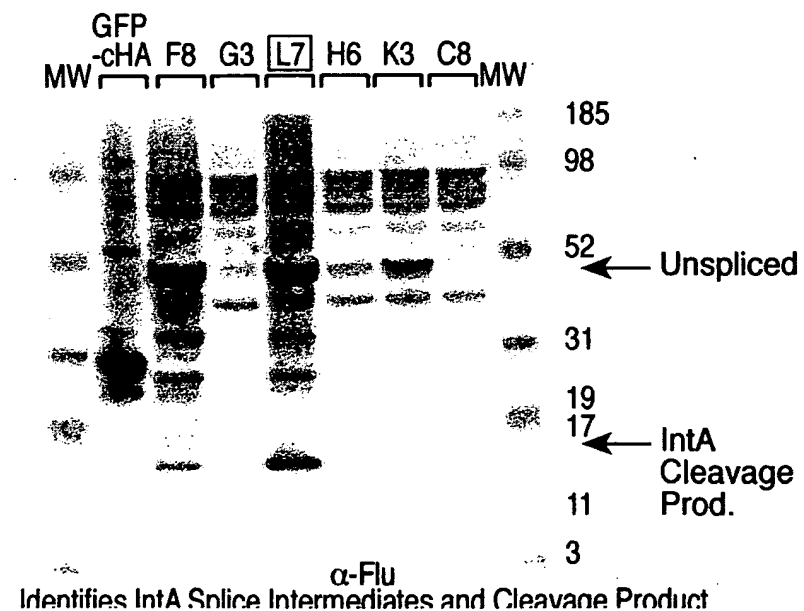
**FIG. 13D-2**

$\alpha$ -myc  
Identifies Only Cyclic Product with Reconstructed Myc Epitope

**FIG. 13D-3**

$\alpha$ -Flu  
Identifies IntA Splice Intermediates and Cleavage Product

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**FIG.\_13D-4****FIG.\_13D-5****FIG.\_13D-6**

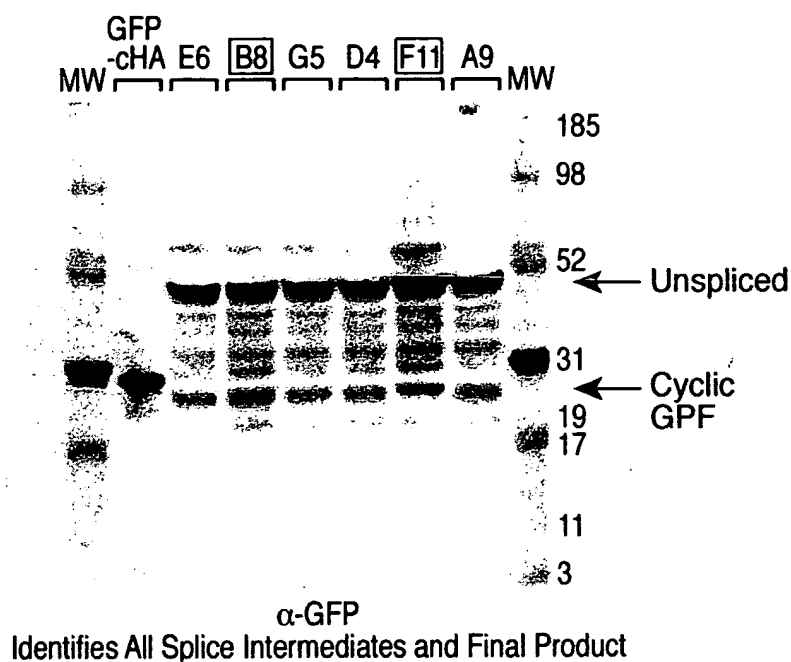


FIG.\_13D-7

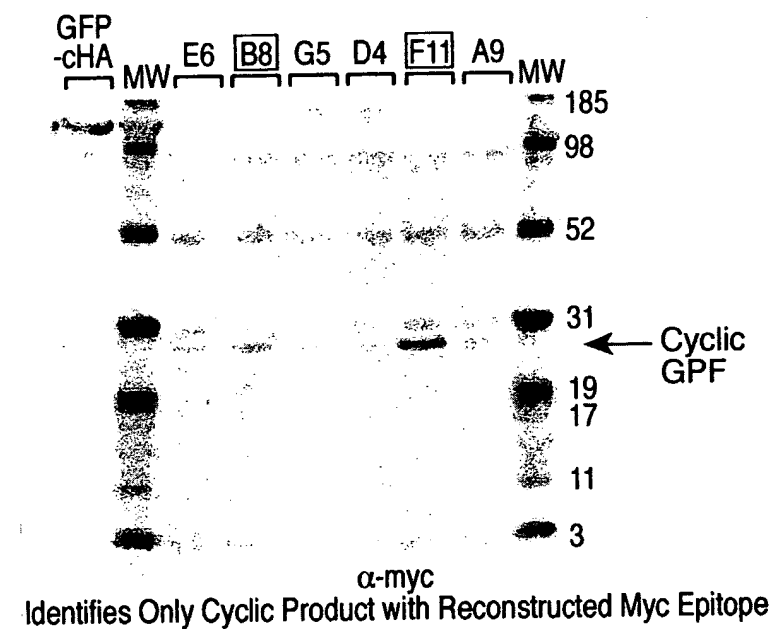


FIG.\_13D-8

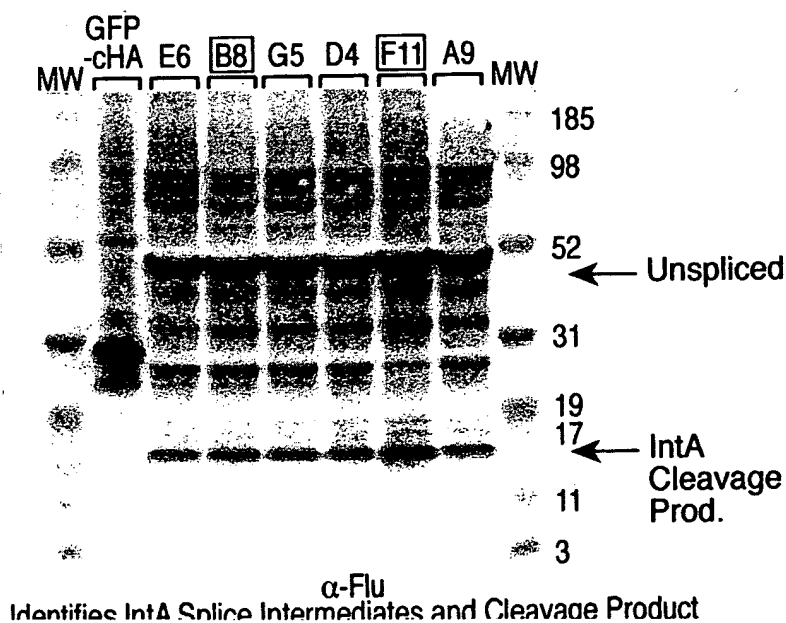


FIG.\_13D-9



Transfected PhxA Cells

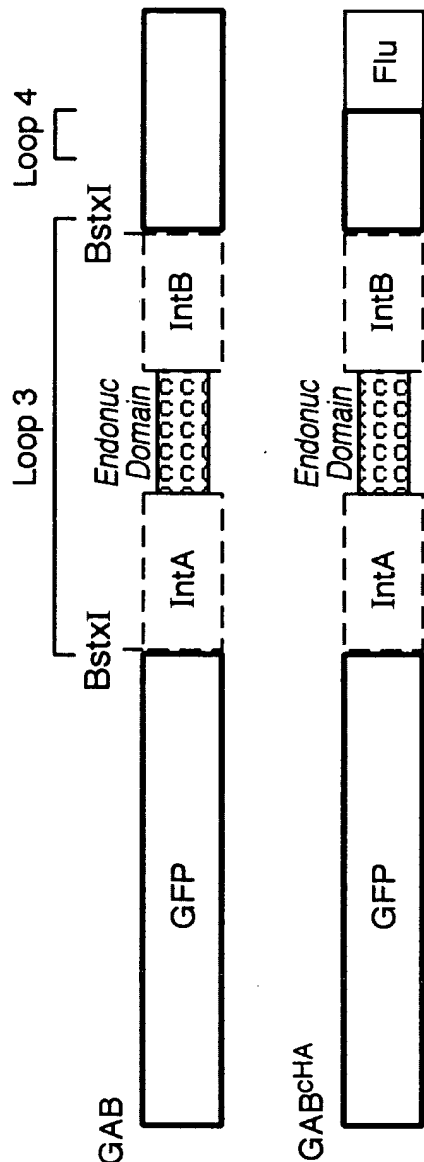
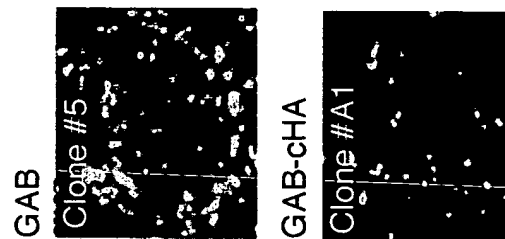


FIG. 14A

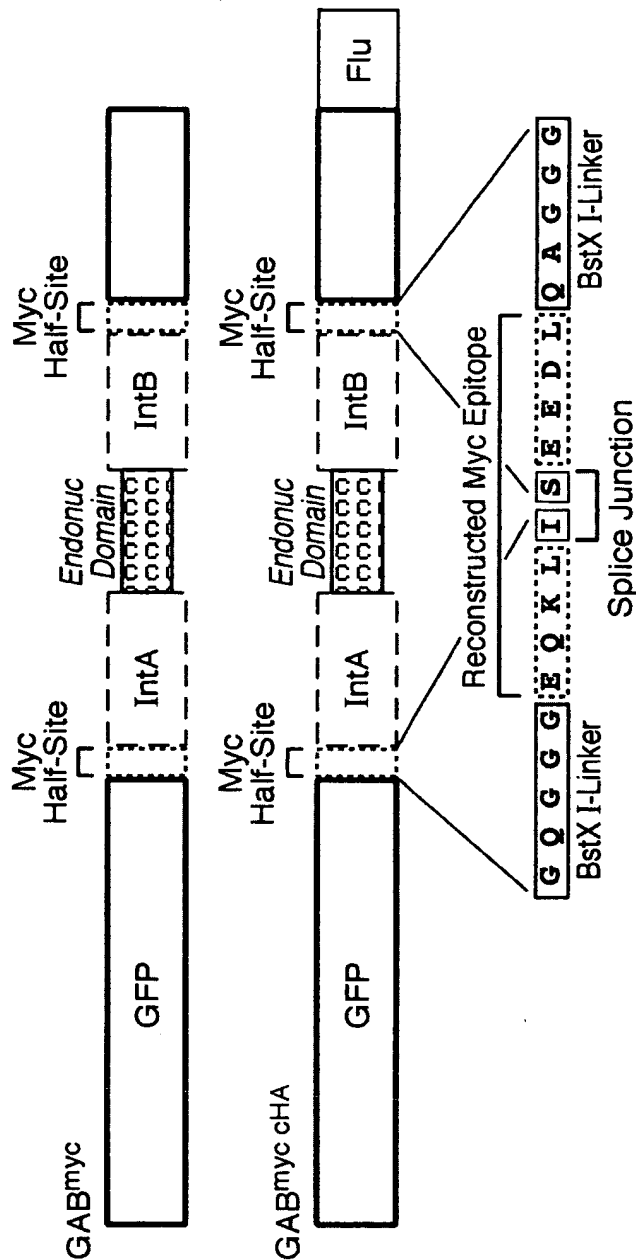
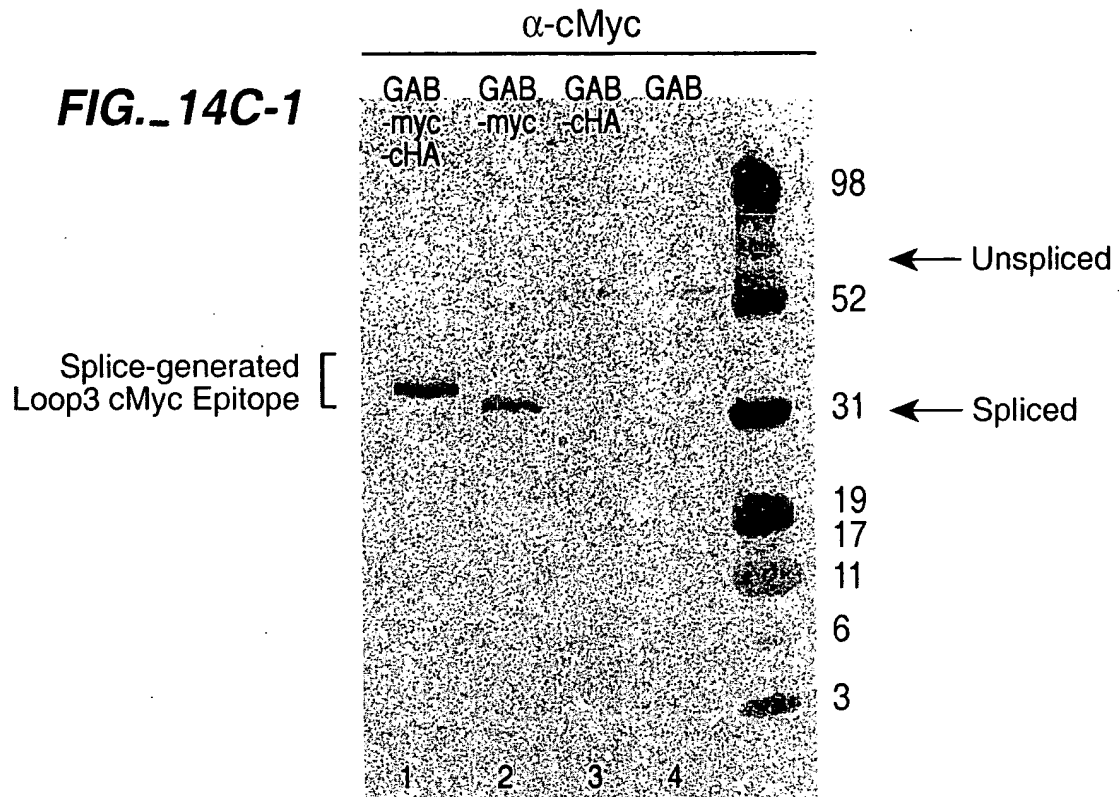
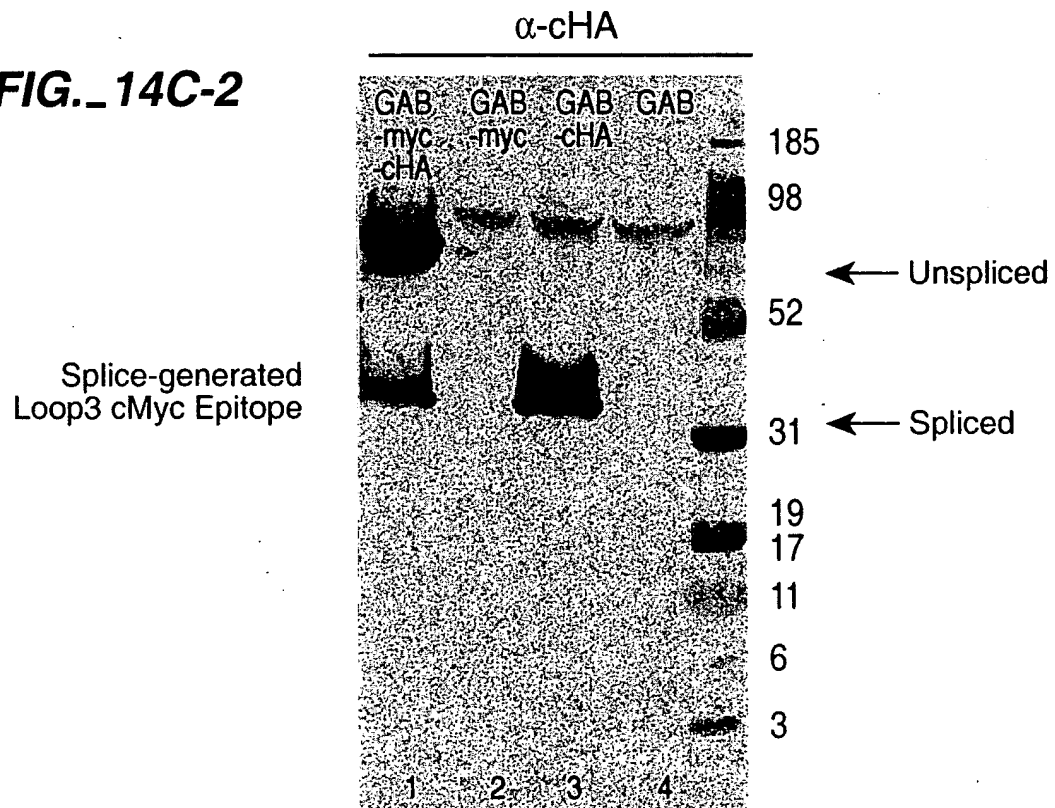
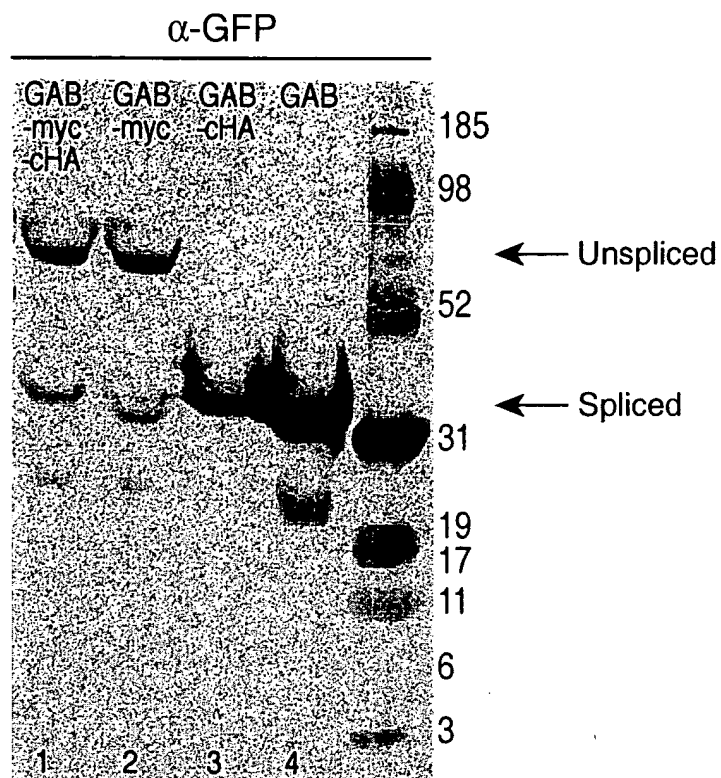
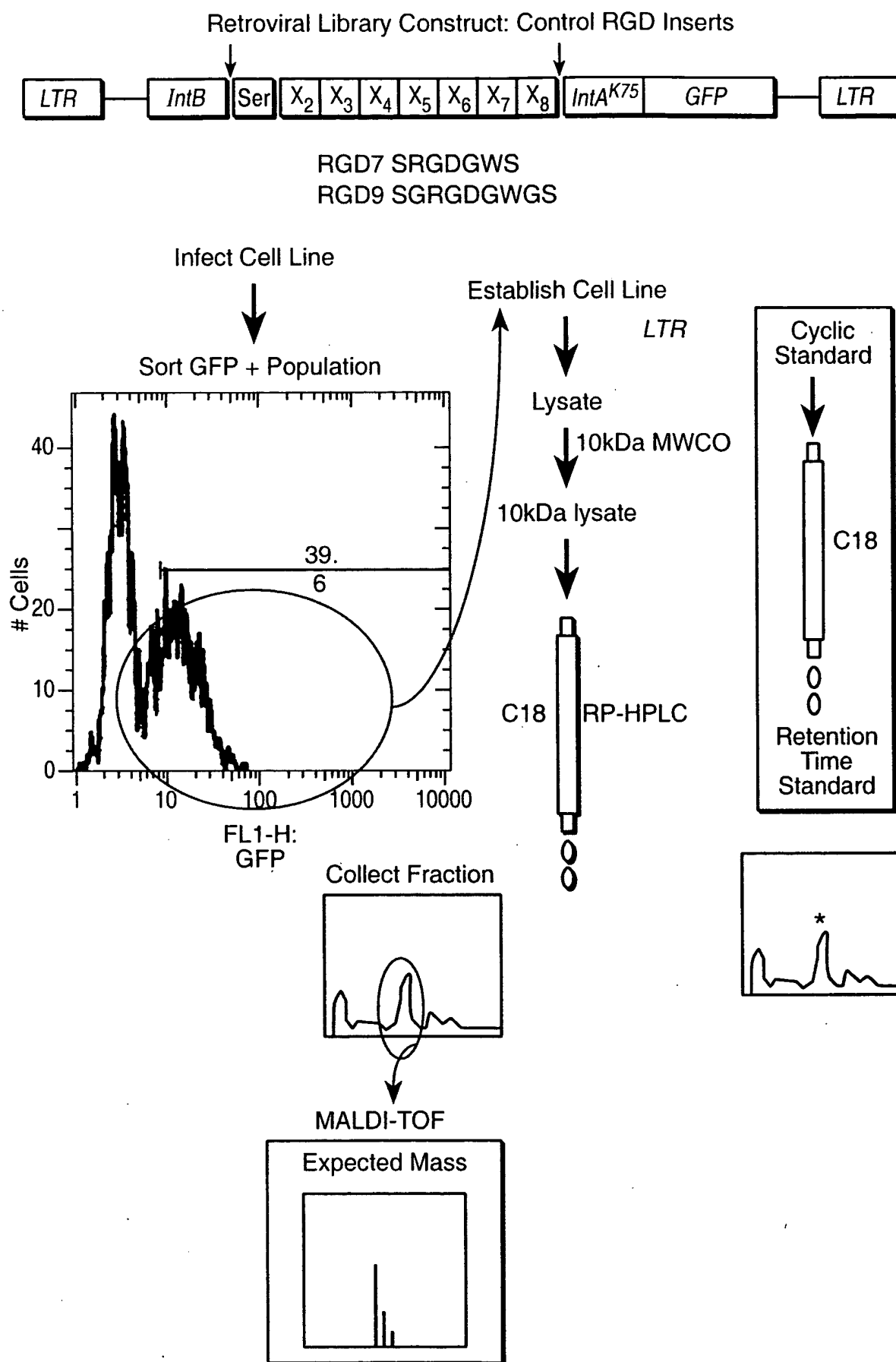


FIG. 14B

**FIG.\_14C-1****FIG.\_14C-2**

**FIG.\_14C-3**Splice-generated  
Loop3 cMyc Epitope [



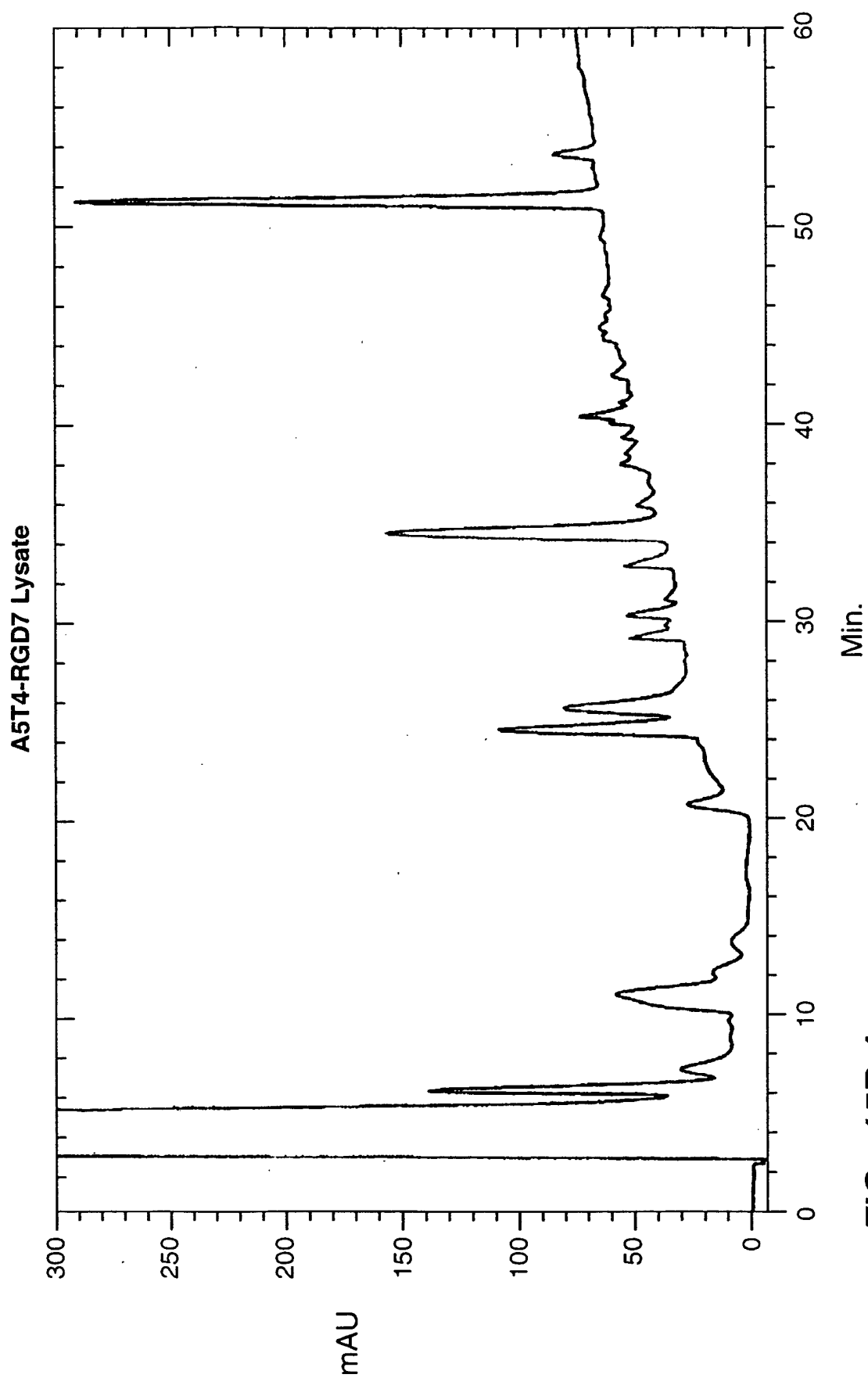
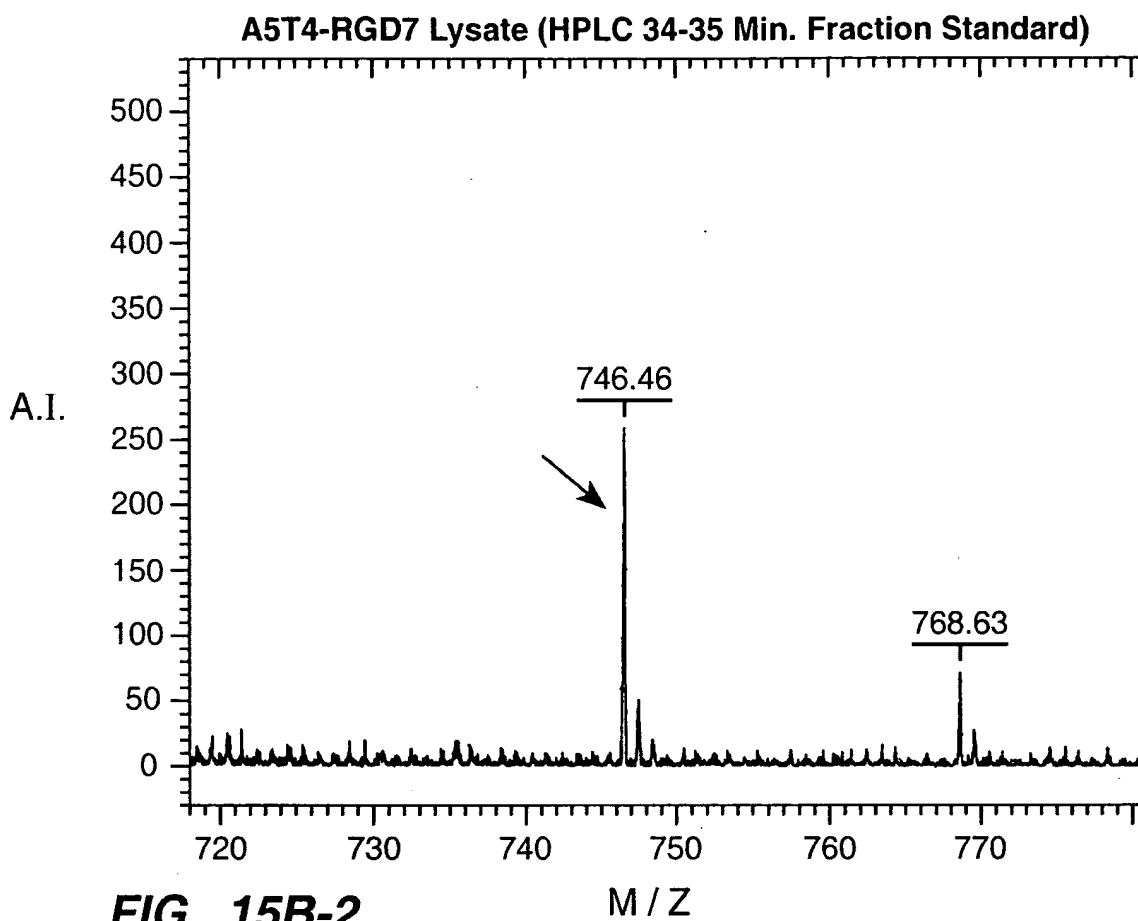
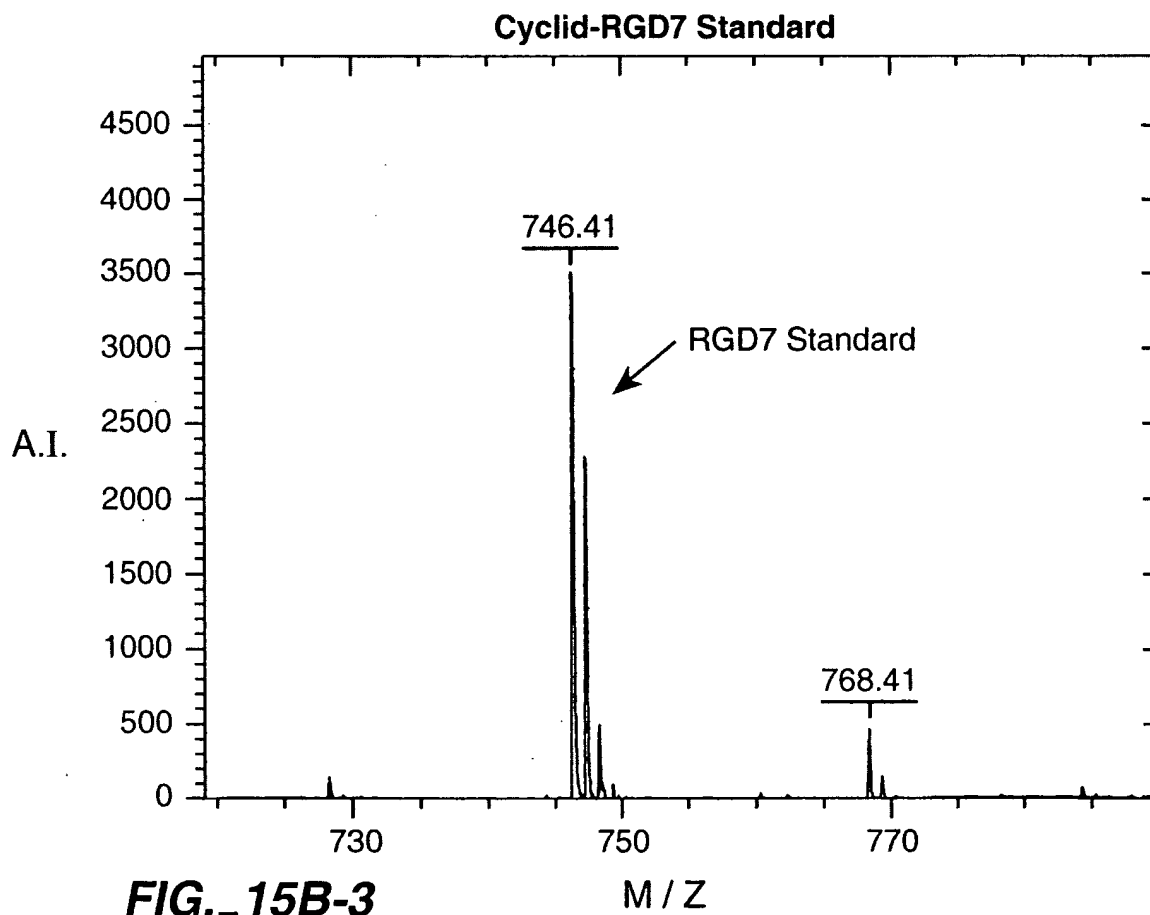
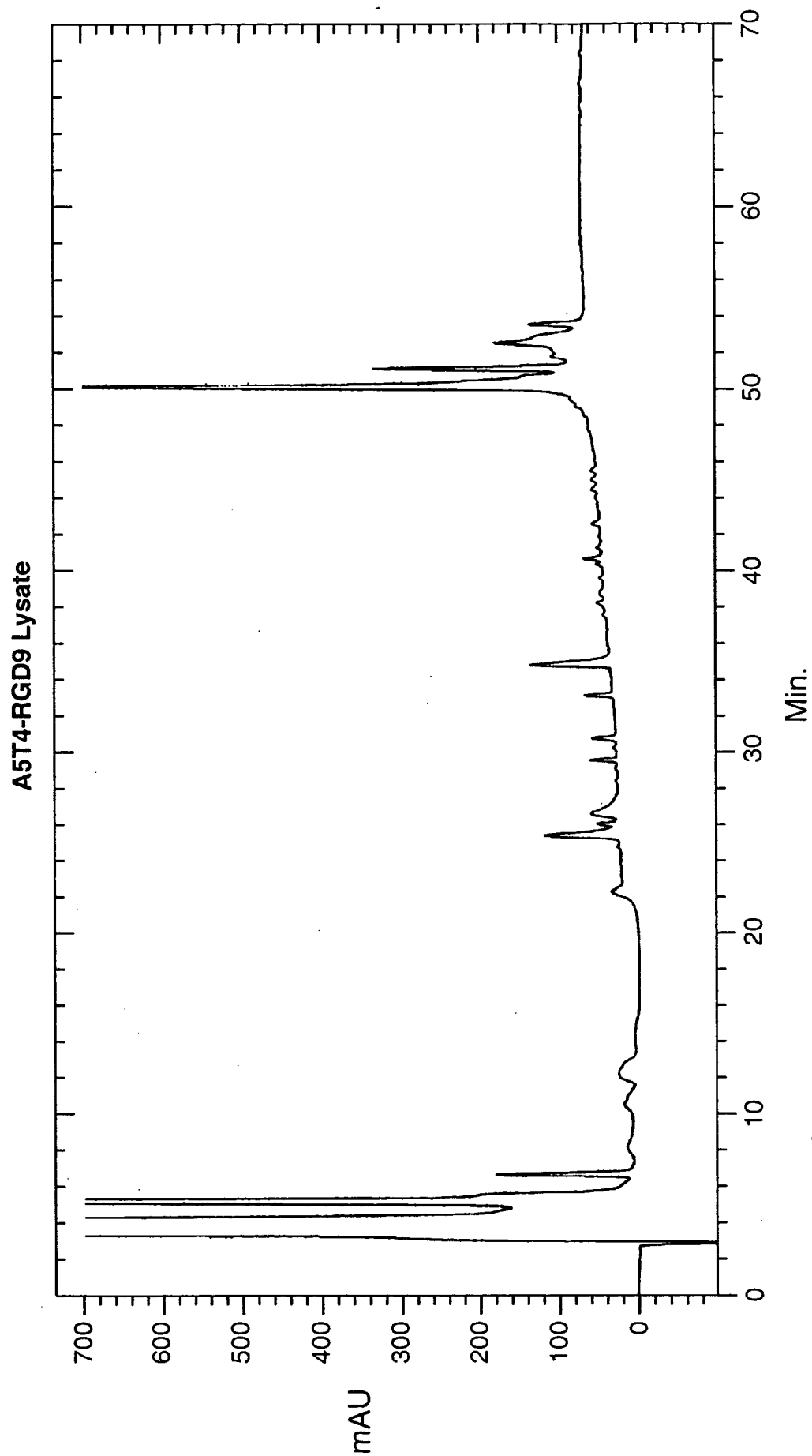


FIG.. 15B-1

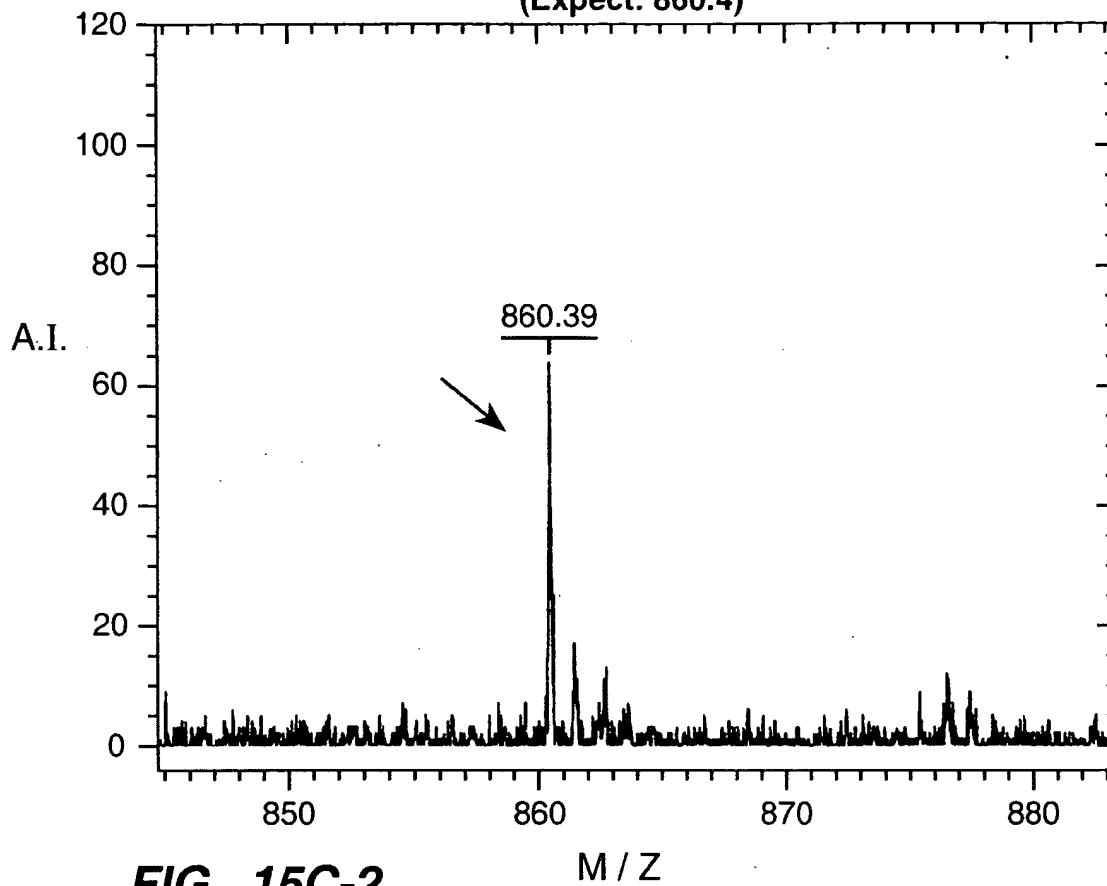
**FIG.\_15B-2****FIG.\_15B-3**

**FIG.\_15C-1**

+

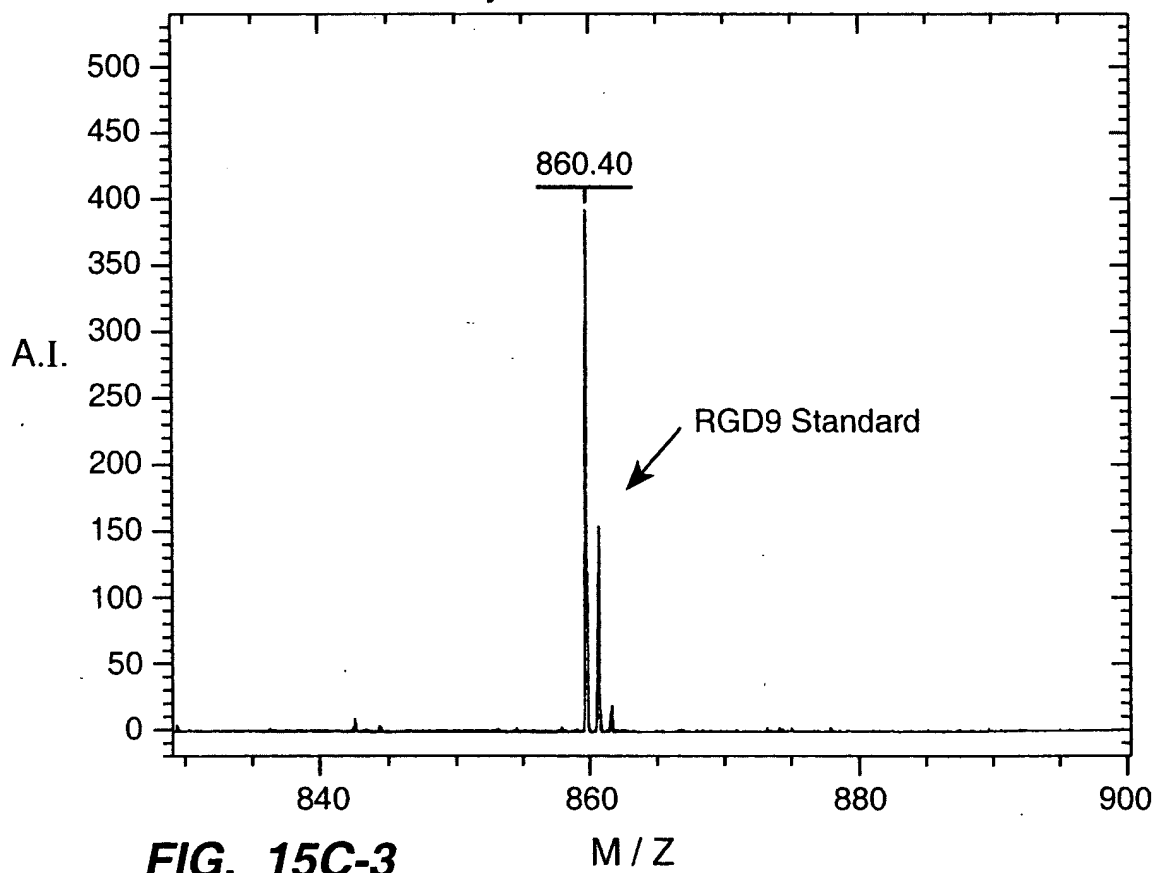
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**A5T4-RGD7 Lysate (HPLC 33-34 Min. Fraction Standard)**  
(Expect: 860.4)



**FIG.\_15C-2**

**Cyclid-RGD9 Standard**



**FIG.\_15C-3**



LC / MS Fragmentation  
Fingerprinting  
RGD7 10kD Lysate  
34-35 Fraction  
15 Major Peaks  
Overlap

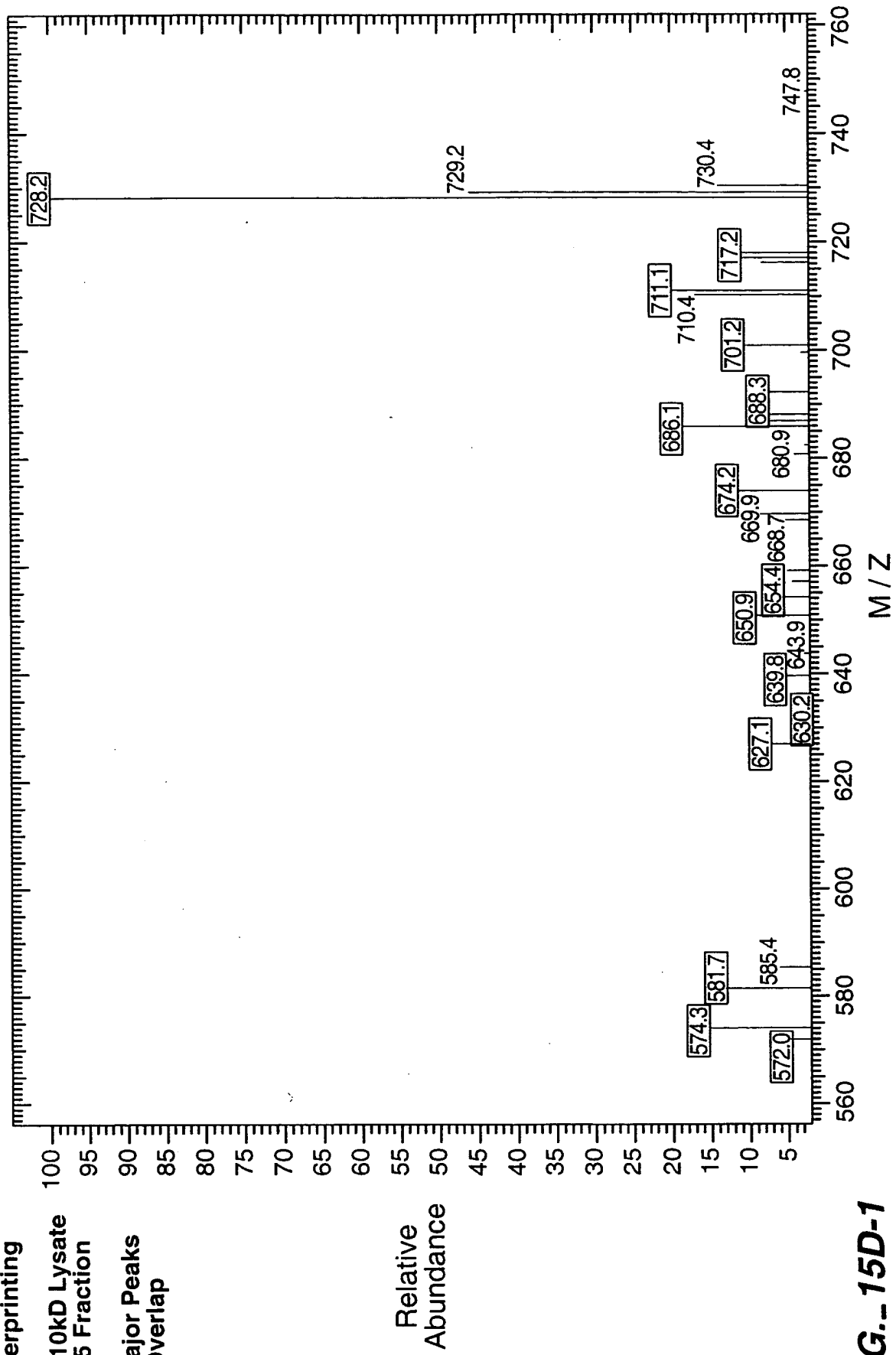


FIG.\_15D-1

## RGD7 Standard

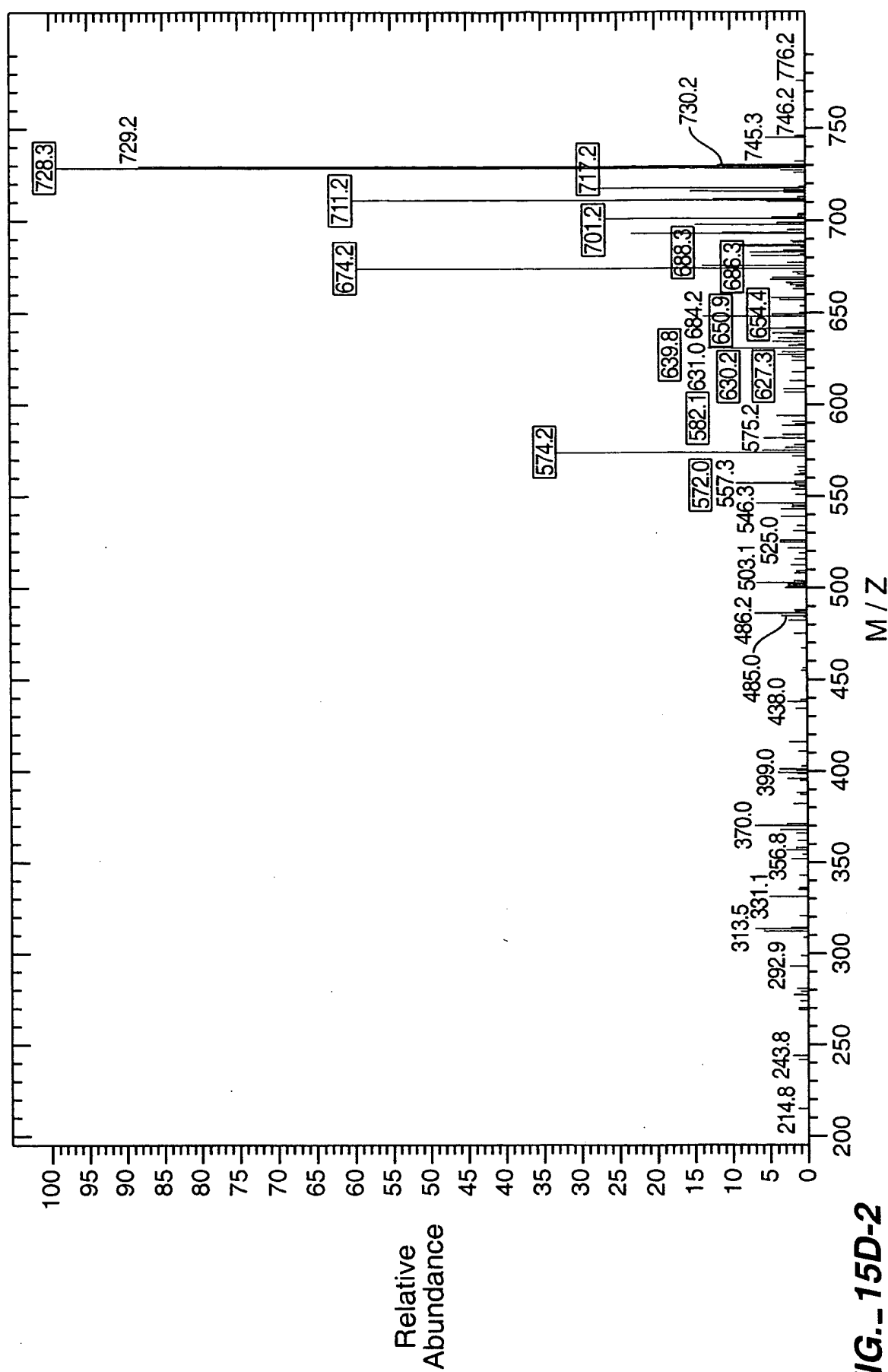


FIG.\_15D-2

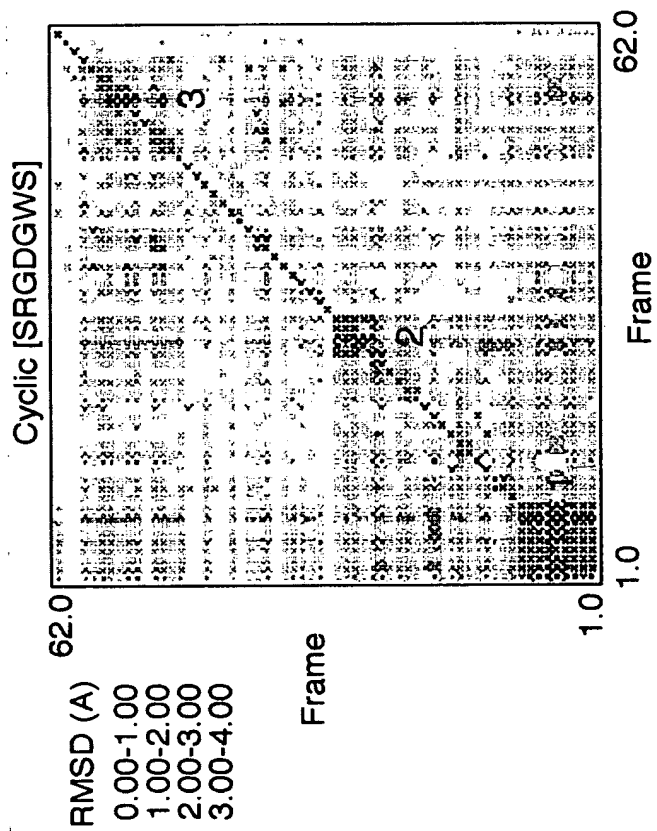


FIG.\_16

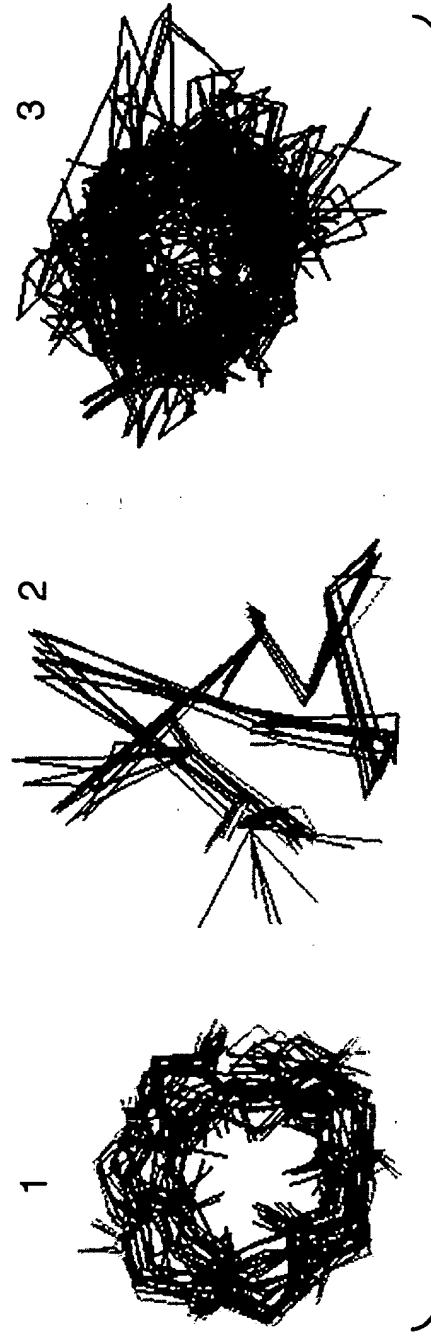
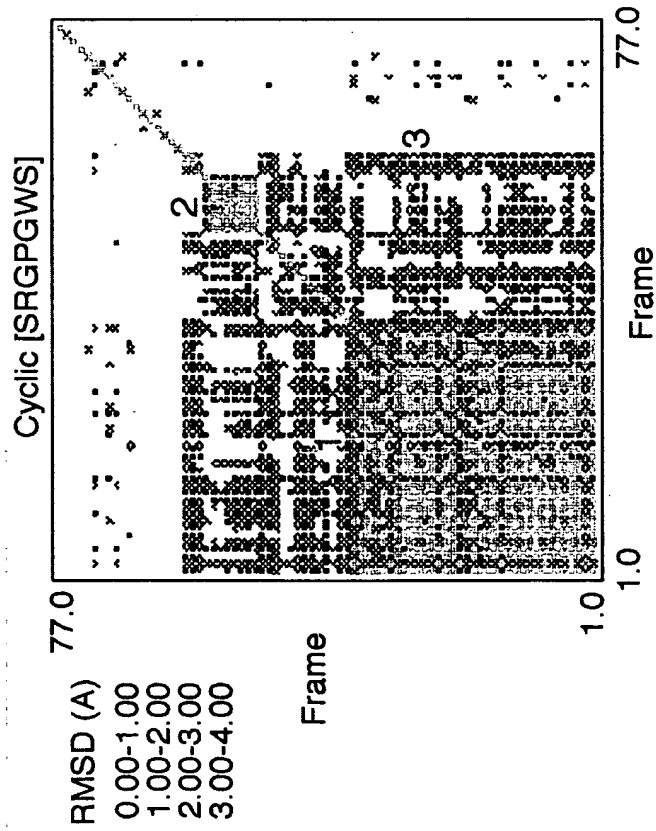


FIG.\_17